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(54) Title: CA125 GENE AND ITS USE FOR DIAGNOSTIC AND THERAPEUTIC INTERVENTIONS

(57) Abstract: The CA125 gene has been cloned and multiple repeat sequences as well as the carboxy terminus have been identified. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. The amino acid composition of the amino terminal extension was found to be consistent with the amino acid composition of the amino terminal domain. The molecular structure is dominated by a repeat domain comprising 156 amino acid repeat units, which encompass the epitope binding sites. More than 60 repeat units have been identified, sequenced, and contiguously placed in the CA125 domain structure. More specifically, this invention is directed to a CA125 cDNA sequence which can be introduced into animal or human cells to achieve transcription or expression of the cDNA.

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## CA125 GENE AND ITS USE FOR DIAGNOSTIC AND THERAPEUTIC INTERVENTIONS

### BACKGROUND OF THE INVENTION

[0001] This application is a continuation-in-part of U.S. Provisional Application Serial No. 60/284,175 filed April 17, 2001, U.S. Provisional Application Serial No. 60/299,380 filed June 19, 2001, U.S. Non-Provisional Application No. 09/965,738 filed September 27, 2001, and U.S. Provisional Application Serial No. 60/345,180. This application is a continuation-in-part of provisional application 60/427,045 (filed November 15, 2002), all of which are hereby specifically incorporated by reference. Applicants hereby specifically claims the benefit of these prior filed applications under 35 U.S.C. § 119(e), and 120.

[0002] The present invention relates generally to the cloning, identification, and expression of the CA125 gene's glycosylated amino terminal domain, the multiple repeat domain, and the carboxy terminal domain *in vitro* and, more specifically, to the use of recombinant CA125 with epitope binding sites for diagnostic and therapeutic purposes. Additionally, the genomic DNA, a molecule encoding a 5' upstream region of CA125 and a genomic DNA sequence for the amino terminal, extra cellular repeats and carboxy terminal of CA125 has been determined.

[0003] CA125 is an antigenic determinant located on the surface of ovarian carcinoma cells with essentially no expression in normal adult ovarian tissue. Elevated in the sera of patients with ovarian adenocarcinoma, CA125 has played a critical role for more than 15 years in the management of these patients relative to their response to therapy and also as an indicator of recurrent disease.

[0004] It is well established that CA125 is not uniquely expressed in ovarian carcinoma, but is also found in both normal secretory tissues and other carcinomas (i.e., pancreas, liver, colon) [Hardardottir H *et al.*, Distribution of CA125 in embryonic tissue and adult derivatives of the fetal periderm, *Am J Obstet. Gynecol.* 163;6(1):1925-1931 (1990); Zurawski VR *et al.*, Tissue distribution and characteristics of the CA125 antigen, *Cancer Rev.* 11-12:102-108 (1988); and O'Brien TJ *et al.*, CA125 antigen in human amniotic fluid and fetal membranes, *Am J Obstet Gynecol.* 155:50-55, (1986); Nap M *et al.*, Immunohistochemical characterization of 22 monoclonal antibodies against the CA125 antigen: 2nd report from the ISOBM TD-1 workshop, *Tumor Biology* 17:325-332 (1996)]. Notwithstanding, CA125 correlates directly with the disease status of affected patients (i.e., progression, regression, and no change), and has become the "gold standard" for monitoring patients with ovarian carcinoma [Bast RC *et al.*, A radioimmunoassay using a monoclonal antibody to monitor the course of epithelial ovarian cancer, *N Engl J Med.* 309:883-887 (1983); and Bon GC *et al.*, Serum tumor marker immunoassays in gynecologic oncology: Establishment of reference values, *Am J Obstet. Gynecol.* 174:107-114 (1996)]. CA125 is especially useful in post-menopausal patients where endometrial tissue has become atrophic and, as a result, is not a major source of normal circulating CA125.

[0005] During the mid 1980's, the inventor of the present invention and others developed M11, a monoclonal antibody to CA125. M11 binds to a dominant epitope on the repeat structure of the CA125 molecule [O'Brien TJ *et al.*, New monoclonal antibodies identify the glycoprotein carrying the CA125 epitope, *Am J Obstet Gynecol* 165:1857-64 (1991)]. More recently, the inventor and others developed a purification and stabilization scheme for CA125, which allows for the accumulation of highly purified high molecular weight CA125 [O'Brien TJ *et al.*, More than 15 years of CA125: What is known about the antigen, its structure and its function, *Int J Biological Markers* 13(4):188-195 (1998)].

[0006] Considerable progress has been made over the years to further characterize the CA125 molecule, its structure and its function. The CA125 molecule is a high molecular weight glycoprotein with a predominance of O-linked sugar side chains. The native molecule exists as a

very large complex (~2-5 million daltons). The complex appears to be composed of an epitope containing CA125 molecule and binding proteins which carry no CA125 epitopes. The CA125 molecule is heterogenous in both size and charge, most likely due to continuous deglycosylation of the side chains during its life-span in bodily fluids. The core CA125 subunit is in excess of 200,000 daltons, and retains the capacity to bind both OC125 and M11 class antibodies.

[0007] Despite the advances in detection and quantitation of serum tumor markers like CA125, the majority of ovarian cancer patients are still diagnosed at an advanced stage of the disease--Stage III or IV. Further, the management of patients' responses to treatment and the detection of disease recurrence remain major problems. There, thus, remains a need to significantly improve and standardize current CA125 assay systems. Further, the development of an early indicator of risk of ovarian cancer will provide a useful tool for early diagnosis and improved prognosis.

#### **SUMMARY OF THE INVENTION**

[0008] Thus, it is an object of the present invention to provide a recombinant CA125 cDNA molecule which can be introduced into animals or human cells to achieve transcription or expression of the cDNA. The utility of knowing the DNA sequence of a specific gene is that a recombinant protein can be produced which can be used as an easily renewable source of that gene or a portion of the gene. Producing and purifying recombinant protein is easier and can produce greater quantities of protein than purifying native protein from patients. The recombinant protein can then be used to produce antibodies to the gene, both polyclonal and monoclonal. The recombinant protein can also be used as a positive control in test kits and experiments.

[0009] The genomic sequence for CA125 and a 5' upstream region has been determined. A DNA sequence showing the 5' upstream region and the amino terminal portion of the CA125 molecule is set out in Table 1 and SEQ ID NO: 1. The extracellular amino terminal domain is made of exons: Exon 1 from 2205-11679; Exon 2 from 13464-13570; Exon 3 from 16177-34419; Exon 4 from 34575-38024; Exon 5 from 38689-38800; Exon 6 from 40578-45257; Exon



7 from 47360-47395; Exon 8 from 52407-52442; Exon 9 from 52686-52744 as set out in SEQ ID NO: 1. A DNA sequence showing the extracellular repeat portion of the CA125 molecule is set out in Table 2 and SEQ ID NO: 2. The genomic repeats are made of exons: Exon R1 from 1-130; Exon R2 from 442-510; Exon R3 from 5479-5652; Exon R4 from 6301-6334; Exon R5 from 6593-6657; Exon R1 from 7558-7683; Exon R2 from 8216-8284; Exon R3 from 8877-9050; Exon R4 from 9380-9413; Exon R5 from 9675-9739; Exon R1 from 10201-10291; Exon R2 from 10524-10592; Exon R3 from 11200-11373; Exon R4 from 11722-11755; Exon R5 from 12016-12036; Exon R1 from 12169-12295; Exon R2 from 12532-12600; Exon R3 from 13219-13392; Exon R4 from 13723-13756; Exon R5 from 14016-14077; Exon R1 from 15001-15126; Exon R2 from 15367-15435; Exon R1 from 15648-15773; Exon R2 from 16002-16070; Exon R3 from 16653-16826; Exon R4 from 17158-17191; Exon R5 from 17453-17517; Exon R1 from 18532-18657; Exon R2 from 18888-18956; Exon R3 from 19633-19806; Exon R4 from 20141-20176; Exon R5 from 20387-20449; Exon R1 from 21609-21731; Exon R2 from 21940-22008; Exon R3 from 22605-22778; Exon R4 from 23109-23142; Exon R1 from 29046-29168; Exon R2 from 29266-29334; Exon R3 from 33917-34090; Exon R4 from 36702-36734; Exon R5 from 38270-38320; Exon R1 from 39104-39224; Exon R2 from 39315-39383; Exon R3 from 39532-39705; Exon R4 from 41862-41992. A DNA sequence showing the carboxy terminal domain of the CA125 molecule is set out in Table 3 and SEQ ID NO: 3. The carboxy terminal portion is made of exons: Exon C1 from 1-66; Exon C2 from 1802-1947; Exon C3 from 4198-4350; Exon C4 from 4679-4747; Exon C5 from 6811-6978; Exon C6 from 11232-11270; Exon C7 from 11594-11677; Exon C8 from 14095-14187 as set out in SEQ ID NO: 3. A full length cDNA molecule for CA125 is set out in Table 4 and SEQ ID NO: 4. A CA125 protein is set out in Table 5 and SEQ ID NO: 5.

**[0010]** Now that the DNA sequence which encodes CA125 has been discovered known synthetic methods can be employed to prepare DNA molecules containing portions of the sequence. Conventional cloning vehicles, such as plasmids, viruses, or bacteria phages can be modified using known methods so as to produce novel cloning vehicles which contain cDNA encoding, CA125, analogs or mutants thereof. Similarly, such cloning vehicles can be modified or engineered so that they contain DNA molecules from Table 4 and SEQ ID NO: 4 or segments

substantially similar thereto. The DNA molecule inserted may be made by various methods including enzymatic or chemical synthesis.

[0011] The CA125 gene has been cloned and multiple repeat sequences as well as the glycosylated amino terminal and the carboxy terminus have been identified. CA125 requires a transcript of more than 35,000 bases and occupies approximately 150,000 bp on chromosome 19p 13.2. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. Analysis of the amino terminal extension revealed that its amino acid composition is consistent with the amino acid composition of the amino terminal domain.

[0012] Perhaps even more significantly, the multiple repeat domains of CA125 or other domains could also be used for the development of a potential vaccine for patients with ovarian cancer. In order to induce cellular and humoral immunity in humans to CA125, murine antibodies specific for CA125 were utilized in anticipation of patient production of anti-ideotypic antibodies, thus indirectly allowing the induction of an immune response to the CA125 molecule. With the availability of recombinant CA125, especially domains which encompass epitope binding sites for known murine antibodies, it will be feasible to more directly stimulate patients' immune systems to CA125 and, as a result, extend the life of ovarian carcinoma patients.

[0013] The recombinant CA125 of the present invention may also be used to develop therapeutic targets. Molecules like CA125, which are expressed on the surface of tumor cells, provide potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. Humanized or human antibodies to CA125 epitopes could be used to deliver all drug or toxic agents including radioactive agents to mediate direct killing of tumor cells. Natural ligands having a natural

binding affinity for domains on the CA125 molecule could also be utilized to deliver therapeutic agents to tumor cells.

[0014] CA125 expression may further provide a survival or metastatic advantage to ovarian tumor cells. Antisense oligonucleotides derived from the CA125 repeat sequences could be used to down-regulate the expression of CA125. Further, antisense therapy could be used in association with a tumor cell delivery system of the type described above.

[0015] Recombinant domains of the CA125 molecule also have the potential to identify small molecules, which bind to individual domains of the CA125 molecule. These small molecules could also be used as delivery agents or as biological modifiers.

[0016] In another aspect of the present invention, an isolated nucleic acid of the CA125 gene is disclosed, which comprises a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequences set forth in SEQ ID NOS: 1, 2, 3 and 4; (b) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (a); (c) a degenerate variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

[0017] In another aspect of the present invention, an isolated nucleic acid of the CA125 gene, comprising a sequence that encodes a polypeptide with the amino acid sequence selected from the group consisting of: (a) the amino acid sequences set forth in SEQ ID NO: 5; (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a); (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

[0018] The vector may be a cloning vector, a shuttle vector, or an expression vector. A cultured cell comprising the vector is also contemplated.

[0019] More specifically, this invention relates to a purified antibody that selectively binds to an epitope in the CA125 protein of SEQ ID NO: 5. Similarly, the purified antibody selectively binds to an amino acid sequence having at least 50% sequence identity to said sequence; the purified antibody selectively binds to an amino acid sequence having at least 60% sequence identity to said sequence; the purified antibody selectively binds to an amino acid sequence

having at least 70% sequence identity to said sequence; the purified antibody selectively binds to an amino acid sequence having at least 80% sequence identity to said sequence; and the purified antibody selectively binds to an amino acid sequence having at least 90% sequence identity to said sequence. Additionally, purified antibody can be a conservative variant of the amino acid sequence set forth in SEQ ID NO: 5 or a fragment thereof.

**DETAILED DESCRIPTION OF THE INVENTION**

[0020] In accordance with the present invention, conventional molecular biology, microbiology, and recombinant DNA techniques may be used that will be apparent to those skilled in the relevant art. Such techniques are explained fully in the literature (see, e.g., Maniatis, Fritsch & Sambrook, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D. N. Glover ed. 1985); "Oligonucleotide Synthesis" (M. J. Gait ed. 1984); "Nucleic Acid Hybridization" (B. D. Hames & S. J. Higgins eds. (1985)); "Transcription and Translation" (B. D. Hames & S. J. Higgins eds. (1984)); "Animal Cell Culture" (R. I. Freshney, ed. (1986)); "Immobilized Cells And Enzymes" (IRL Press, (1986)); and B. Perbal, "A Practical Guide To Molecular Cloning" (1984)).

[0021] Therefore, if appearing herein, the following terms shall have the definitions set out below.

[0022] A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

[0023] A "DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in either single stranded form, or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, inter alia, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes.

[0024] As used herein, the term "gene" shall mean a region of DNA encoding a polypeptide chain.

[0025] "Messenger RNA" or "mRNA" shall mean an RNA molecule that encodes for one or more polypeptides.

[0026] "DNA polymerase" shall mean an enzyme which catalyzes the polymerization of deoxyribonucleotide triphosphates to make DNA chains using a DNA template.

[0027] "Reverse transcriptase" shall mean an enzyme which catalyzes the polymerization of deoxy- or ribonucleotide triphosphates to make DNA or RNA chains using an RNA or DNA template.

[0028] "Complementary DNA" or "cDNA" shall mean the DNA molecule synthesized by polymerization of deoxyribonucleotides by an enzyme with reverse transcriptase activity.

[0029] An "isolated nucleic acid" is a nucleic acid the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs; (b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein.

[0030] "Oligonucleotide", as used herein in referring to the probes or primers of the present invention, is defined as a molecule comprised of two or more deoxy- or ribonucleotides, preferably more than ten. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

[0031] "DNA fragment" includes polynucleotides and/or oligonucleotides and refers to a plurality of joined nucleotide units formed from naturally-occurring bases and cyclofuranosyl groups joined by native phosphodiester bonds. This term effectively refers to naturally-occurring species or synthetic species formed from naturally-occurring subunits. "DNA fragment" also refers to purine and pyrimidine groups and moieties which function similarly but which have non naturally-occurring portions. Thus, DNA fragments may have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other

sulfur containing species. They may also contain altered base units or other modifications, provided that biological activity is retained. DNA fragments may also include species which include at least some modified base forms. Thus, purines and pyrimidines other than those normally found in nature may be so employed. Similarly, modifications on the cyclofuranose portions of the nucleotide subunits may also occur as long as biological function is not eliminated by such modifications.

[0032] "Primer" shall refer to an oligonucleotide, whether occurring naturally or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, the source of primer and the method used. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 10-25 or more nucleotides, although it may contain fewer nucleotides.

[0033] The primers herein are selected to be "substantially" complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence or hybridize therewith and thereby form the template for the synthesis of the extension product.

[0034] As used herein, the term "hybridization" refers generally to a technique wherein denatured RNA or DNA is combined with complementary nucleic acid sequence which is either

free in solution or bound to a solid phase. As recognized by one skilled in the art, complete complementarity between the two nucleic acid sequences is not a pre-requisite for hybridization to occur. The technique is ubiquitous in molecular genetics and its use centers around the identification of particular DNA or RNA sequences within complex mixtures of nucleic acids.

[0035] As used herein, "restriction endonucleases" and "restriction enzymes" shall refer to bacterial enzymes which cut double-stranded DNA at or near a specific nucleotide sequence.

[0036] "Purified polypeptide" refers to any peptide generated from CA125 either by proteolytic cleavage or chemical cleavage.

[0037] "Degenerate variant" refers to any amino acid variation in the repeat sequence, which fulfills the homology exon structure and conserved sequences and is recognized by the M11, OC125 and ISOBM series of antibodies.

[0038] "Fragment" refers to any part of the CA125 molecule identified in a purification scheme.

[0039] "Conservative variant antibody" shall mean any antibody that fulfills the criteria of M11, OC125 or any of the ISOBM antibody series.

[0040] "Homology" refers to similarity based on identical base matches in alignment. When two sequences are identical there is a 100% homology, as base matches differ in alignment the homology between two sequences is reduced.

[0041] The CA125 gene has been cloned and multiple repeat sequences as well as the carboxy terminus have been identified. The genomic DNA for the CA125 gene is set out in SEQ ID NO: 4. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity



for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. The amino acid composition of the amino terminal extension was found to be consistent with the amino acid composition of the amino terminal domain. The molecular structure is dominated by a repeat domain comprising 156 amino acid repeat units, which encompass the epitope binding sites. More than 60 repeat units have been identified, sequenced, and contiguously placed in the CA125 domain structure. The repeat units encompass an interactive disulfide bridged C-enclosure and the site of OC125 and M11 binding. The repeat sequences demonstrated 70-85% homology to each other. Expression of the repeats was demonstrated in *E. coli*. The CA125 molecule is anchored at its carboxy terminal through a transmembrane domain and a short cytoplasmic tail. The carboxy terminal also contains a proteolytic cleavage site approximately 50 amino acids upstream from the transmembrane domain, which allows for proteolytic cleavage and release of the CA125 molecule. Any one of the repeat domains has the potential for use as a new gold standard for detecting and monitoring the presence of the CA125 antigen. Further, the repeat domains or other domains, especially the c-terminal to the repeat domain also provide a basis for the development of a vaccine, which would be useful for the treatment of ovarian cancer and other carcinomas where CA125 is elevated.

[0042] The DNA sequences of the present invention can also be characterized as encoding the amino acid sequence equivalents of the amino acid sequence, equivalents, as used in this context, include peptides of substantially similar length and amino acid identity to those disclosed, but having conservative amino acid substitution at a non-critical residue position. A conservative amino acid substitution is a substitution in which an amino acid residue is replaced with an amino acid residue of differing identity, but whose R group can be characterized by chemically similar. Four common categories include: polar but uncharged R groups; positively charged R groups; negatively charged R groups; and, hydrophobic R groups. A preferred conservative substitution involves the substitution of a second hydrophobic residue for a first hydrophobic residue, the first and second hydrophobic residues differing primarily in the size of the R group. The hydrophobic residue would be predicted to be located internally in the folded peptide structure and the mild perturbation caused only by a change in the size of an R group at

an internally located which would not alter the antigenicity of R protein. More specifically, two nucleic acid molecules are substantially equivalent if they have at least about 70% homology.

[0043] The isolated cDNA sequences (Table 4 and SEQ ID NO: 4) of the present invention can be inserted into an expression vector. Such vectors contain all necessary regulatory signals to promote the expression of a DNA sequence of interest. Expression vectors are typically either prokaryote or eukaryote specific. Expression vectors can be introduced into either prokaryote or eukaryote cells to produce CA125 proteins or portions thereof. The isolated cDNA sequence as shown in Table 4 was expressed to provide the CA125 molecule set out in Table 5 and SEQ ID NO: 5. The expressed CA125 is a polypeptide with the amino acid sequence set forth in SEQ ID NO: 5; an amino acid sequence having at least 50% sequence identity to the sequence, a conservative for variant or a fragment of any of the above. Two polypeptide sequences are substantially equivalent if there is at least 50% sequence homology and substantial similar physical characteristics. However, in practice, a portion of an isolated nucleic acid molecule set out in SEQ ID NO: 4 is expressed to obtain a fragment of the CA125 molecule. This fragment is then purified to obtain an isolated CA125 fragment.

[0044] In certain embodiments, "purified" refers to a polypeptide composition which has been subjected to fractionation to remove various nonprotein components such as other cellular components. Various techniques suitable for use in protein purification are known to those skilled in the relevant art. These techniques include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like or by heat denaturation, followed by centrifugation; chromatography steps such as ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combination of such techniques. Similarly, a "purification scheme" is a technique or system to remove various nonprotein components such as other cellular components from the expressed protein. Various techniques suitable for use in protein purification are known to those skilled in the relevant art. These techniques include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like or by heat denaturation, followed by centrifugation; chromatography steps such as

ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combination of such techniques.

[0045] The genomic DNA and a full-length cDNA sequence of human CA125 has been determined. Additionally, a nucleic acid molecule encoding a 5' upstream region of the CA125 gene has been determined. cDNA is expressed with the use of an expression vector. An expression vector is a carrying vector that has an inducer for expression built into the vector. Different vectors use different inducers. The cDNA is ligased into the expression vector using restriction digest sites designed in the vector. The cDNA must be ligased in the sense direction and in the correct reading frame for expression to occur. Once the cDNA is ligased into the expression vector, the construct is transformed into a cell. In the preferred embodiment, we use E-Coli bacteria, but the transformation can be done with yeast, mammalian cells, plants cells, etc. The transformed cells are then grown in culture and protein production is induced with the an inducing agent for the expression vector. In the preferred embodiment, we use the pQE-30 expression vector and induce with IPTG. Once induction has occurred, the cells are harvested and the protein is purified. It should be noted that some expression vectors add tags to the recombinant protein to aid in purification. For example, pQE-30 adds a His-Tag which binds to nickel to aid in purification. Once cells have been successfully transformed, a small aliquot can be frozen and stored for future use.

[0046] With a cDNA sequence, one skilled in the art has an easily renewable source of purified CA125. Portions of this cDNA sequence can be expressed to make CA125 polypeptides and these polypeptides can be used to make monoclonal antibodies. These monoclonal antibodies can be made by one skilled in the art to portions of the protein which heretofore do not have any monoclonal antibodies, such as the amino terminal sequence.

[0047] More specifically, the purified antibodies are made by the following process: the recombinant protein is injected into an animal (usually a mouse, but other animals can be used). The animal's B-lymphocytes produce antibodies to the protein. Each activated B lymphocyte forms a clone of cells in spleen or lymph nodes, with each cell of the clone producing identical antibody. These spleen cells are then harvested and fused with myeloma cells to produce

hybridomas. These hybridomas are immortal and produce only one type of antibody. The hybridomas are selected from cells that did not fuse by selective media. The hybridomas can then be grown in large quantities to produce large quantities of monoclonal antibodies.

**[0048]**     **Therapeutic Targets:** Molecules, which are expressed on the surface of tumor cells as CA125 is, offer potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. CA125 offers such potential as a target: 1) Antibodies to CA125 epitopes or newly described potential epitopes: Most especially humanized or human antibodies to CA125 which could directly activate the patients' immune system to attack and kill tumor cells. Antibodies could be used to deliver all drug or toxic agents including radioactive agents to mediate direct killing of tumor cells. 2) Natural ligands: Under normal circumstances, molecules are bound to the CA125 molecule e.g. a 50 k dalton protein which does not contain CA125 epitopes co-purifies with CA125. Such a molecule, which might have a natural binding affinity for domains on the CA125 molecule, could also be utilized to deliver therapeutic agents to tumor cells.

**[0049]**     **Anti-sense therapy:** CA125 expression may provide a survival or metastatic advantage to ovarian tumor cells as such antisense oligonucleotide derived from the CA125 sequence could be used to down-regulate the expression of CA125. Antisense therapy could be used in association with a tumor cell delivery system such as described above.

**[0050]**     **Small Molecules:** Recombinant domains of CA125 also offer the potential to identify small molecules which bind to individual domains of the molecule. Small molecules either from combinatorial chemical libraries or small peptides can also be used as delivery agents or as biological modifiers.

**[0051]**     **Transgenic Animals/Transformed:** CA125 and genomic DNA can be used to develop transgenic animal models and can be used under low stringency conditions, to clone CA125 cDNAs and genomic DNAs of other animal species. The CA125 cDNA can be used to prepare stable transformants. The bacterial cells could be transformed with CA125 cDNA to include these genes.

**Example 1**

[0052] Expression of 6xHis-tagged CA125 repeat in E. coli: The open reading frame of the CA125 repeat was amplified by PCR with the 5' sense primer 1 (5'-ACCGGATCCATGGGCCACACAGAGCCTGGCCC-3') (SEQ ID NO: 6) and the 3' antisense primer 2 (5'-TGTAAGCTTAGGCAGGGAGGATGGAGTCC-3') (SEQ ID NO: 7). The open reading frame of the CA125 repeat constitutes a portion of the isolated nucleic acid molecule set out in SEQ ID NO: 4. PCR was performed in a reaction mixture consisting of ovarian tumor cDNA derived from 50 ng of mRNA, 5 pmol each of sense and antisense primers for the CA125 repeat, 0.2 mmol of dNTPs, and 0.625 U of Taq polymerase in 1x buffer in a final volume of 25  $\mu$ l. This mixture was subjected to 1 minute of denaturation at 95°C followed by 30 cycles of PCR consisting of the following: denaturation for 30 seconds at 95°C, 30 seconds of annealing at 62°C, and 1 minute of extension at 72°C with an additional 7 minutes of extension on the last cycle. The product was electrophoresed through a 2% agarose gel for separation, the PCR product was purified and digested with the restriction enzymes BamHI and HindIII. This digested PCR product was ligated into the expression vector pQE-30, which had also been digested with BamHI and HindIII. The ligation reaction consisted of 1ul of 10x ligation buffer, 1ul of 10x bovine serum albumin (BSA), 1ul of T4 ligase enzyme, and 7ul of digested PCR product. The reaction went overnight at 15° C. This clone would allow for expression of recombinant amino-terminal 6xHis-tagged CA125 repeat. The construct was then transformed into JM109 E. coli cells. The transformation reaction consisted of 5ul of ligation reaction and 50ul of cells. The reaction was mixed gently and then incubated on ice for 30 minutes. The reaction was then heat shocked at 42° C for 45 seconds in a water bath before being returned to ice for 2 minutes. 500ul of LB broth media were added and the mixture was incubated at 37° C for 1 hour. At the end of 1 hour the cells were spun down in a microfuge at 4,000 x g for 5 minutes and approximately 450ul of media was removed. The cells were resuspended in the remaining 100ul of media, transferred to a LAIX plate, and incubated overnight at 37° C. White colonies were picked from the plate and cultured in 5ml LB broth media to determine if the transformation was successful. Transformed E. coli were grown in 1L cultures to an OD<sub>600</sub> of 1.5-2.0 at 37°C and were induced with IPTG (0.1 mM) for 4-6 hours at 25°C to produce

recombinant protein. Whole E.coli lysate was electrophoresed through a denaturing 12% polyacrylamide gel and Coomassie stained to detect highly expressed proteins. His-tagged proteins were purified under denaturing conditions using Ni-NTA agarose metal chelating affinity chromatography available from Qiagen according to the manufacturer's instructions. Cells are spun down to remove liquid LB broth media. The cells are then resuspended in 40ml of 8M Urea lysis buffer (pH 8.0) and incubated with agitation overnight at room temperature. The mixture is then spun down and the lysate is removed. The lysate is then incubated with Ni-NTA agarose beads with agitation overnight at room temperature. The beads are pelleted and the supernatant is removed. The beads are then washed twice in lysis buffer pH 8.0 plus Triton X, three times with lysis buffer pH 6.3 plus Triton X, and four times with lysis buffer pH 6.3 without Triton X. The protein is then eluted from the beads with lysis buffer pH4.2 plus 25mM EDTA incubated overnight with agitation at room temperature. The beads are pelleted and the supernatant containing the recombinant protein is removed. The supernatant is then dialyzed twice in .2x PBS to remove the urea and freeze dried for storage. 1L of culture produced 2.4mg of recombinant protein.

**[0053]** It should be understood that various changes and modifications to the presently preferred embodiments described herein will be apparent to those skilled in the art. Such changes and modifications can be made without departing from the spirit and scope of the present invention and without diminishing its attendant advantages.

Table 1

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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1 GGTGCGCACC ACTATGTCTG GCTAATTTTT GTATTTTTTT GTAGAGACAT  
51 GGTTCACCA TGTGGCCAG GCTGGTCTCG AATTCCTGAC TTCAAGTAAT  
101 CCACCCACCT CAGCCTCCCA AAGTGCTGGG ATTACAAGCA TGAGCCACCA  
151 TGCATGGCCT AAAGCTTCTT TTAAAGCCAC CAAGTCCCTT CCCATGTTAG  
201 CCCACTAATC CATGGGTTAG TCATGAATGG ATTAATCTAT TCATACGGAC  
251 AGAGCCCTCA TCACCCAATC ACCTCTTAAA GGCCCCACCT CTCAATACTG  
301 CCACACTGGG GATTAAGTTT CAACAGAGTT TTGGAGGGGA CATTCAAATC  
351 ATAGTAATGC CCAAAGTGAA AAATCTTCCC TGCACTTTTT CCTCAACAAA  
401 AACAGCCAGA GATAGTGAGC TGCCAGGAAA TTCTTTTTTT TTTCCTCTTC  
451 TGTCTAAAT CAGCATCGCT AGACCTTTAC ATGATTCAAC CTCATCTTCT  
501 TCACCCTCTG GGTCTGTAAG TTTTATTTAT TTATTTATTA TTTTCTGGG  
551 ACAGACTCTG GCTCTGTCGC CCAGGCTGAA GTGCAGTGGT GTGATCTTGG  
601 CTCCTGCAA CCTCCGCCTC CCGGGTTCAA GCGATTCTCC TGCCTCAGCC  
651 TCCTGAGTAG CTGGGATTAC AGGTGGGCGC CACCACACCC AGCTAATTTT  
701 TTGTATTTTT AGTAGAGATG GGGTTTCACC ATATTAGCCA GGATGGTCTC  
751 CATCTCTTGA CCTCGTGATC TGCCACCTC AGCCTCCCA AATGCTGGGA  
801 TTACAGGCAT GAGACACCAC GCCCAGCAGG CCAGGGTCAT GAGATTTTAA  
851 TCAAGAGCAA CTTCCACTGA TTCCTGAGAG TGCATCTGTG GGCCCTGCT  
901 CTGATCTGAA CAGAAGTGCC GTGTCTTCTC TGACCTCCAC TTCTCAATTC  
951 AAGAGCCTTA GTATCTGCCA GTATCACACA CTGAGCATTG GCTCCATCTC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)				
1001	ATGGGGGTGT	AGGTAGGGGC	TCTATCTGCA	TCTTTCTTTC
	TTTTTTTCTT			
1051	TCTTTCCCTT	CCTCCCTTCC	TCCTCCCTC	GGTCCTCTCT
	TTCTTTCCCT			
1101	TTCTTTCTTC	CTTCCTCCCT	TCCTCCCTCC	CTCCCTCTCT
	CTTTCTCTCT			
1151	TTCTTTCTTT	CCTTCTTTCT	TTCTTTCTCT	CTTCCTTCCC
	TCCCTCCCTC			
1201	CTTCCTTCCT	TTCTCTTTCT	TTCTCTTTCT	TTCTTTTTTT
	CCTTCCTTCC			
1251	TTCTTTCTTT	CTCTTTCTCT	CCCTCCCTTC	CTTCCTTCCT
	TCCTTCCTTC			
1301	CTTCCTTTCT	TTCTTTCTTT	CTTTCTTTCT	TTCTTTCTTT
	CTTTCTTTCT			
1351	TTCTTTCTTC	CTTCCTTCCT	TCCTTCCTTC	CTTCCTTCCT
	TCCTTCCTTT			
1401	CTTTTCTTTC	TTTCTCTTTC	TTTTTGAGAC	AGAGCTCTTA
	TTACCCATGC			
1451	TGGAGTGCAG	TGGTGTGACC	TTGGCTTACT	GCAACATCTG
	CCTCCTAGGG			
1501	TCAAGTGATT	CTCCTGCCTC	AGCCTCCTAA	GTAGCTGGGA
	TTACAGACAC			
1551	ATGCCACCAC	ACCCAATATT	TATTTTTATT	AAAATTTTTT
	TTAAAAATTAT			
1601	TTTTAAAAAA	TTAAAAATAA	TTTTGTATTT	TTAGTAGAGA
	CGGGGTTTCT			
1651	CCATGTTGGT	CAGGCTGATC	TCAAACCTCC	AACCTCAGGT
	GATCCTCCCA			
1701	CCTCACCTCC	CAAAGTGCTG	GGATTACAGG	CATGAGCCAC
	CGTGCCCAGC			
1751	CTGGTTCCTG	GTTTCTAAGA	CATCACACAC	ACACACACAC
	ACACACACAC			
1801	ACACTCACAC	ACTCAGAGAG	AGAGAGAGAG	AGAGGATCAT
	TAAGACATGA			
1851	TACACTAAGA	AATTCTATTC	TGCAGACACT	GAGAATCCGT
	TAAAAAGTTT			
1901	GAAGGGAAGA	ATTGAGATCA	TCAGGTGTTT	ATTTGAGGAA
	ATTGTCTGTG			
1951	GTTGAACTAT	CCTTTCCTTT	CTCTCCCTGA	GATTTGGTCT
	TCTCAATTAG			



Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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2001 AAGCGTTGCA CAATTCCTCCC AACCTCCATA CATACGGCAG CTCTTCTAGA  
 2051 CACAGGTTTT CCCAGGTCAA ATGCGGGGAC CCCAGCCATA TCTCCCACCC  
 2101 TGAGAAATTT TGGAGTTTCA GGGAGCTCAG AAGCTCTGCA GAGGCCACCC  
 2151 TCTCTGAGGG GATTCTTCTT AGACCTCCAT CCAGAGGCAA ATGTTGACCT

**Exon1**

2201 GTCCATGCTG AAACCCTCAG GCCTTCCTGG GTCATCTTCT CCCACCCGCT  
 2251 CCTTGATGAC AGGGAGCAGG AGCACTAAAG CCACACCAGA AATGGATTCA  
 2301 GGACTGACAG GAGCCACCTT GTCACCTAAG ACATCTACAG GTGCAATCGT  
 2351 GGTGACAGAA CATACTCTGC CCTTTACTTC CCCAGATAAG ACCTTGGCCA  
 2401 GTCCTACATC TTCGGTTGTG GGAAGAACCA CCCAGTCTTT GGGGGTGATG  
 2451 TCCTCTGCTC TCCCTGAGTC AACCTCTAGA GGAATGACAC ACTCCGAGCA  
 2501 AAGAACCAGC CCATCGCTGA GTCCCAGGT CAATGGTACT CCCTCTAGGA  
 2551 ACTACCCTGC TACAAGCATG GTTTCAGGAT TGAGTTCCCC AAGGACCAGG  
 2601 ACCAGTTCCA CAGAAGGAAA TTTTACCAA GAAGCATCTA CATAACACT  
 2651 CACTGTAGAG ACCACAAGTG GCCCAGTCAC TGAGAAGTAC ACAGTCCCCA  
 2701 CTGAGACCTC AACAACTGAA GGTGACAGCA CAGAGACCCC CTGGGACACA  
 2751 AGATATATTC CTGTAAAAAT CACATCTCCA ATGAAAACAT TTGCAGATTC  
 2801 AACTGCATCC AAGGAAAATG CCCCAGTGTC TATGACTCCA GCTGAGACCA  
 2851 CAGTTACTGA CTCACATACT CCAGGAAGGA CAAACCCATC ATTTGGGACA  
 2901 CTTTATTCTT CCTTCCTTGA CCTATCACCT AAAGGGACCC CAAATTCAG

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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2951 AGGTGAAACA AGCCTGGAAC TGATTCTATC AACCACTGGA TATCCCTTCT  
3001 CCTCTCCTGA ACCTGGCTCT GCAGGACACA GCAGAATAAG TACCAGTGCG  
3051 CCTTTGTCAT CATCTGCTTC AGTTCTCGAT AATAAAATAT CAGAGACCAG  
3101 CATATTCTCA GGCCAGAGTC TCACCTCCCC TCTGTCTCCT GGGGTGCCCC  
3151 AGGCCAGAGC CAGCACAATG CCCAACTCAG CTATCCCTTT TTCCATGACA  
3201 CTAAGCAATG CAGAAACAAG TGCCGAAAGG GTCAGAAGCA CAATTTCCTC  
3251 TCTGGGGACT CCATCAATAT CCACAAAGCA GACAGCAGAG ACTATCCTTA  
3301 CCTTCCATGC CTTCGCTGAG ACCATGGATA TACCCAGCAC CCACATAGCC  
3351 AAGACTTTGG CTTCAGAATG GTTGGGAAGT CCAGGTACCC TTGGTGGCAC  
3401 CAGCACTTCA GCGCTGACAA CCACATCTCC ATCTACCACT TTAGTCTCAG  
3451 AGGAGACCAA CACCCATCAC TCCACGAGTG GAAAGGAAAC AGAAGGAACT  
3501 TTGAATACAT CTATGACTCC ACTTGAGACC TCTGCTCCTG GAGAAGAGTC  
3551 CGAAATGACT GCCACCTTGG TCCCCACTCT AGGTTTTACA ACTCTTGACA  
3601 GCAAGATCAG AAGTCCATCT CAGGTCTCTT CATCCCACCC AACAGAGAG  
3651 CTCAGAACCA CAGGCAGCAC CTCTGGGAGG CAGAGTTCCA GCACAGCTGC  
3701 CCACGGGAGC TCTGACATCC TGAGGGCAAC CACTTCCAGC ACCTCAAAG  
3751 CATCATCATG GACCAGTGAA AGCACAGCTC AGCAATTTAG TGAACCCAG  
3801 CACACACAGT GGGTGGAGAC AAGTCCTAGC ATGAAAACAG AGAGACCCCC  
3851 AGCATCAACC AGTGTGGCAG CCCCTATCAC CACTTCTGTT CCCTCAGTGG  
3901 TCTCTGGCTT CACCACCCTG AAGACCAGCT CCACAAAAGG GATTGGCTT

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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3951 GAAGAAACAT CTGCAGACAC ACTCATCGGA GAATCCACAG CTGGCCCAAC  
4001 CACCCATCAG TTTGCTGTTC CCACTGGGAT TTCAATGACA GGAGGCAGCA  
4051 GCACCAGGGG AAGCCAGGGC ACAACCCACC TACTCACCAG AGCCACAGCA  
4101 TCATCTGAGA CATCCGAGA TTTGACTCTG GCCACGAACG GTGTCCCAGT  
4151 CTCCGTGTCT CCAGCAGTGA GCAAGACGGC TGCTGGCTCA AGTCCTCCAG  
4201 GAGGGACAAA GCCATCATAT ACAATGGTTT CTTCTGTCAT CCCTGAGACA  
4251 TCATCTCTAC AGTCCTCAGC TTTCAGGGAA GGAACCAGCC TGGGACTGAC  
4301 TCCATTAAAC ACTAGACATC CCTTCTCTTC CCCTGAACCA GACTCTGCAG  
4351 GACACACCAA GATAAGCACC AGCATTCCTC TGTTGTCATC TGCTTCAGTT  
4401 CTTGAGGATA AAGTGTGAGC GACCAGCACA TTCTCACACC ACAAAGCCAC  
4451 CTCATCTATT ACCACAGGGA CTCCTGAAAT CTCAACAAAG ACAAAGCCCA  
4501 GCTCAGCCGT TCTTTCCTCC ATGACCCTAA GCAATGCAGC AACAAGTCCT  
4551 GAAAGAGTCA GAAATGCAAC TTCCCCTCTG ACTCATCCAT CTCCATCAGG  
4601 GGAAGAGACA GCAGGGAGTG TCCTCACTCT CAGCACCTCT GCTGAGACTA  
4651 CAGACTCACC TAACATCCAC CCAACTGGGA CACTGACTTC AGAATCGTCA  
4701 GAGAGTCCTA GCACTCTCAG CCTCCCAAGT GTCTCTGGAG TCAAACCAC  
4751 ATTTTCTTCA TCTACTCCTT CCACTCATCT ATTTACTAGT GGAGAAGAAA  
4801 CAGAGGAAAC TTCGAATCCA TCTGTGTCTC AACCTGAGAC TTCTGTTTCC  
4851 AGAGTAAGGA CCACCTTGGC CAGCACCTCT GTCCCTACCC CAGTATTCCC  
4901 CACCATGGAC ACCTGGCCTA CAGGTTGAGC TCAGTTCTCT TCATCCCACC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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4951 TAGTGAGTGA GCTCAGAGCT ACGAGCAGTA CCTCAGTTAC AAACTCAACT  
5001 GGTTCAGCTC TTCCTAAAAT ATCTCACCTC ACTGGGACGG CAACAATGTC  
5051 ACAGACCAAT AGAGACACGT TTAATGACTC TGCTGCACCC CAAAGCACAA  
5101 CTTGGCCAGA GACTAGTCCC AGATTCAAGA CAGGGTTACC TTCAGCAACA  
5151 ACCACTGTTT CAACCTCTGC CACTTCTCTC TCTGCTACTG TAATGGTCTC  
5201 TAAATTCACT TCTCCAGCAA CTAGTTCCAT GGAAGCAACT TCTATCAGGG  
5251 AACCATCAAC AACCATCCTC ACAACAGAGA CCACGAATGG CCCAGGCTCT  
5301 ATGGCTGTGG CTTCTACCAA CATCCCAATT GGAAAGGGCT ACATTACTGA  
5351 AGGAAGATTG GACACAAGCC ATCTGCCCAT TGAACCACA GCTTCCTCTG  
5401 AGACATCTAT GGATTTTACC ATGGCCAAAG AAAGTGTCTC AATGTCAGTA  
5451 TCTCCATCTC AGTCCATGGA TGCTGCTGGC TCAAGCACTC CAGGAAGGAC  
5501 AAGCCAATTC GTTGACACAT TTTCTGATGA TGTCTATCAT TTAACATCCA  
5551 GAGAAATTAC AATACCTAGA GATGGAACAA GCTCAGCTCT GACTCCACAA  
5601 ATGACTGCAA CTCACCCTCC ATCTCCTGAT CCTGGCTCTG CTAGAAGCAC  
5651 CTGGCTTGGC ATCTTGTCCT CATCTCCTTC TTCTCCTACT CCCAAAGTCA  
5701 CAATGAGCTC CACATTTTCA ACTCAGAGAG TCACCACAAG CATGATAATG  
5751 GACACAGTTG AAAC TAGTCG GTGGAACATG CCCAACTTAC CTTCCACGAC  
5801 TTCTTGACA CCAAGTAATA TTCCAACAAG TGGTGCCATA GGAAAAGCA  
5851 CCCTGGTTCC CTTGGACACT CCATCTCCAG CCACATCATT GGAGGCATCA  
5901 GAAGGGGGAC TTCCAACCCT CAGCACCTAC CCTGAATCAA CAAACACACC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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5951 CAGCATCCAC CTCGGAGCAC ACGCTAGTTC AGAAAGTCCA AGCACCATCA  
6001 AACTTACCAT GGCTTCAGTA GTAAACCTG GCTCTTACAC ACCTCTCACC  
6051 TTCCCCTCAA TAGAGACCCA CATTATGTA TCAACAGCCA GAATGGCTTA  
6101 CTCTTCTGGG TCTTCACCTG AGATGACAGC TCCTGGAGAG ACTAACACTG  
6151 GTAGTACCTG GGACCCACAC ACCTACATCA CCACTACGGA TCCTAAGGAT  
6201 ACAAGTTCAG CTCAGGTCTC TACACCCAC TCAGTGAGGA CACTCAGAAC  
6251 CACAGAAAAC CATCCAAAGA CAGAGTCCGC CACCCAGCT GCTTACTCTG  
6301 GAAGTCCTAA AATCTCAAGT TCACCCAATC TCACCAGTCC GGCCACAAAA  
6351 GCATGGACCA TCACAGACAC AACTGAACAC TCCACTCAAT TACATTACAC  
6401 AAAATTGGCA GAAAAATCAT CTGGATTGTA GACACAGTCA GCTCCAGGAC  
6451 CTGTCTCTGT AGTAATCCCT ACCTCCCCTA CCATTGGAAG CAGCACATTG  
6501 GAACTAACTT CTGATGTCCC AGGGGAACCC CTGGTCCTTG CTCCCAGTGA  
6551 GCAGACCACA ATCACTCTCC CCATGGCAAC ATGGCTGAGT ACCAGTTTGA  
6601 CAGAGGAAAT GGCTTCAACA GACCTTGATA TTTCAAGTCC AAGTTCACCC  
6651 ATGAGTACAT TTGCTATTTT TCCACCTATG TCCACACCTT CTCATGAACT  
6701 TTCAAAGTCA GAGGCAGATA CCAGTGCCAT TAGAAATACA GATTCAACAA  
6751 CGTTGGATCA GCACCTAGGA ATCAGGAGTT TGGGCAGAAC TGGGGACTTA  
6801 ACAACTGTTC CTATCACCCC ACTGACAACC ACGTGGACCA GTGTGATTGA  
6851 ACACTCAACA CAAGCACAGG ACACCCTTTC TGCAACGATG AGTCCTACTC  
6901 ACGTGACACA GTCACTCAA GATCAAACAT CTATACCAGC CTCAGCATCC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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6951 CCTTCCCATC TTACTGAAGT CTACCCTGAG CTCGGGACAC AAGGGAGAAG  
7001 CTCCTCTGAG GCAACCACTT TTTGGAAACC ATCTACAGAC ACACTGTCCA  
7051 GAGAGATTGA GACTGGCCCA ACAAACATTC AATCCACTCC ACCCATGGAC  
7101 AACACAACAA CAGGGAGCAG TAGTAGTGGA GTCACCCTGG GCATAGCCCA  
7151 CCTTCCCATA GGAACATCCT CCCAGCTGA GACATCCACA AACATGGCAC  
7201 TGGAAAGAAG AAGTTCTACA GCCACTGTCT CTATGGCTGG GACAATGGGA  
7251 CTCCTTGTTA CTAGTGCTCC AGGAAGAAGC ATCAGCCAGT CATTAGGAAG  
7301 AGTTTCCTCT GTCCTTTCTG AGTCAACTAC TGAAGGAGTC ACAGATTCTA  
7351 GTAAGGGAAG CAGCCCAAGG CTGAACACAC AGGGAAATAC AGCTCTCTCC  
7401 TCCTCTCTTG AACCCAGCTA TGCTGAAGGA AGCCAGATGA GCACAAGCAT  
7451 CCCTCTAACC TCATCTCCTA CAACTCCTGA TGTGGAATTC ATAGGGGGCA  
7501 GCACATTTTG GACCAAGGAG GTCACCACAG TTATGACCTC AGACATCTCC  
7551 AAGTCTTCAG CAAGGACAGA GTCCAGCTCA GCTACCCTTA TGTCCACAGC  
7601 TTTGGGAAGC ACTGAAAATA CAGGAAAAGA AAAACTCAGA ACTGCCTCTA  
7651 TGGATCTTCC ATCTCCAACCT CCATCAATGG AGGTGACACC ATGGATTTCT  
7701 CTCACTCTCA GTAATGCCCC CAATACCACA GATTCACCTG ACCTCAGCCA  
7751 TGGGGTGCAC ACCAGCTCTG CAGGGACTTT GGCCACTGAC AGGTCATTGA  
7801 ATACTGGTGT CACTAGAGCC TCCAGATTGG AAAACGGCTC TGATACCTCT  
7851 TCTAAGTCCC TGTCTATGGG AAACAGCACT CAACTTCCA TGACTTACAC  
7901 AGAGAAGAGT GAAGTGTCTT CTTCAATCCA TCCCCGACCT GAGACCTCAG

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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7951 CTCCTGGAGC AGAGACCACT TTGACTTCCA CTCCTGGAAA CAGGGCCATA  
8001 AGCTTAACAT TGCCTTTTTT ATCCATTCCA GTGGAAGAAG TCATTTCTAC  
8051 AGGCATAACC TCAGGACCAG ACATCAACTC AGCACCCATG ACACATTCTC  
8101 CCATCACCCC ACCAACAATT GTATGGACCA GTACAGGCAC AATTGAACAG  
8151 TCCACTCAAC CACTACATGC AGTTTCTTCA GAAAAAGTTT CTGTGCAGAC  
8201 ACAGTCAACT CCATATGTCA ACTCTGTGGC AGTGTCTGCT TCCCCTACCC  
8251 ATGAGAATTC AGTCTCTTCT GGAAGCAGCA CATCCTCTCC ATATTCCTCA  
8301 GCCTCACTTG AATCCTTGGA TTCCACAATC AGTAGGAGGA ATGCAATCAC  
8351 TTCCTGGCTA TGGGACCTCA CTACATCTCT CCCCACTACA ACTTGGCCAA  
8401 GTACTAGTTT ATCTGAGGCA CTGTCCTCAG GCCATTCTGG GGTTCAAAC  
8451 CCAAGTTCAA CTACGACTGA ATTTCCACTC TTTTCAGCTG CATCCACATC  
8501 TGCTGCTAAG CAAAGAAATC CAGAAACAGA GACCCATGGT CCCCAGAATA  
8551 CAGCCGCGAG TACTTTGAAC ACTGATGCAT CCTCGGTCAC AGGTCTTTCT  
8601 GAGACTCCTG TGGGGGCAAG TATCAGCTCT GAAGTCCCTC TTCCAATGGC  
8651 CATAACTTCT AGATCAGATG TTTCTGGCCT TACATCTGAG AGTACTGCTA  
8701 ACCCGAGTTT AGGCACAGCC TCTTCAGCAG GGACCAAATT AACTAGGACA  
8751 ATATCCCTGC CCACTTCAGA GTCTTTGGTT TCCTTTAGAA TGAACAAGGA  
8801 TCCATGGACA GTGTCAATCC CTTTGGGGTC CCATCCAAC ACTAATACAG  
8851 AAACAAGCAT CCCAGTAAAC AGCGCAGGTC CACCTGGCTT GTCCACAGTA  
8901 GCATCAGATG TAATTGACAC ACCTTCAGAT GGGGCTGAGA GTATTCACAC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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8951 TGTCTCCTTT TCCCCCTCCC CTGATACTGA AGTGACAACT ATCTCACATT  
9001 TCCCAGAAAA GACAACTCAT TCATTTAGAA CCATTTCATC TCTCACTCAT  
9051 GAGTTGACTT CAAGAGTGAC ACCTATTCCT GGGGATTGGA TGAGTTCAGC  
9101 TATGTCTACA AAGCCCACAG GAGCCAGTCC CTCCATTACA CTGGGAGAGA  
9151 GAAGGACAAT CACCTCTGCT GCTCCAACCA CTTCCCCCAT AGTTCTCACT  
9201 GCTAGTTTCA CAGAGACCAG CACAGTTTCA CTGGATAATG AAACCTACGT  
9251 AAAAACCTCA GATATCCTTG ACGCACGGAA AACAAATGAG CTCCCCTCAG  
9301 ATAGCAGTTC TTCTTCTGAT CTGATCAACA CCTCCATAGC TTCTTCAACT  
9351 ATGGATGTCA CTAAACAGC CTCCATCAGT CCCACTAGCA TCTCAGGAAT  
9401 GACAGCAAGT TCCTCCCCAT CTCTCTTCTC TTCAGATAGA CCCCAGGTTC  
9451 CCACATCTAC AACAGAGACA AATACAGCCA CCTCTCCATC TGTTTCCAGT  
9501 AACACCTATT CTCTTGATGG GGGCTCCAAT GTGGGTGGCA CTCCATCCAC  
9551 TTTACCACCC TTTACAATCA CCCACCCTGT CGAGACAAGC TCGGCCCTAT  
9601 TAGCCTGGTC TAGACCAGTA AGAACTTTCA GCACCATGGT CAGCACTGAC  
9651 ACTGCCTCCG GAGAAAATCC TACCTCTAGC AATTCTGTGG TGACTTCTGT  
9701 TCCAGCACCA GGTACATGGA CCAGTGTAGG CAGTACTACT GACTTACCTG  
9751 CCATGGGCTT TCTCAAGACA AGTCCTGCAG GAGAGGCACA CTCACTTCTA  
9801 GCATCAACTA TTGAACCAGC CACTGCCTTC ACTCCCCATC TCTCAGCAGC  
9851 AGTGGTCACT GGATCCAGTG CTACATCAGA AGCCAGTCTT CTCACTACGA  
9901 GTGAAAGCAA AGCCATTCAT TCTTCACCAC AGACCCCAAC TACACCCACC



Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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9951 TCTGGAGCAA ACTGGGAAAC TTCAGCTACT CCTGAGAGCC TTTTGGTAGT  
10001 CACTGAGACT TCAGACACAA CACTTACCTC AAAGATTTTG GTCACAGATA  
10051 CCATCTTGTT TTCAACTGTG TCCACGCCAC CTTCTAAATT TCCAAGTACG  
10101 GGGACTCTGT CTGGAGCTTC CTTCCCTACT TTA CTCCCGG ACACTCCAGC  
10151 CATCCCTCTC ACTGCCACTG AGCCAACAAG TTCATTAGCT ACATCCTTTG  
10201 ATTCCACCCC ACTGGTGACT ATAGCTTCGG ATAGTCTTGG CACAGTCCCA  
10251 GAGACTACCC TGACCATGTC AGAGACCTCA AATGGTGATG CACTGGTTCT  
10301 TAAGACAGTA AGTAACCCAG ATAGGAGCAT CCCTGGAATC ACTATCCAAG  
10351 GAGTAACAGA AAGTCCACTC CATCCTTCTT CCACTTCCCC CTCTAAGATT  
10401 GTTGCTCCAC GGAATACAAC CTATGAAGGT TCGATCACAG TGGCACTTTC  
10451 TACTTTGCCT GCGGGAATA CTGGTTCCCT TGTATT CAGT CAGAGTTCTG  
10501 AAAACTCAGA GACAACGGCT TTGGTAGACT ATCAGCIGG GCTTGAGAGG  
10551 GCATCTGTGA TGCCACTAAC CACAGGAAGC CAGGGTATGG CTAGCTCTGG  
10601 AGGAATCAGA AGTGGGTCCA CTCCTCAAC TGGAACCAAA ACATTTTCTT  
10651 CTCTCCCTCT GACCATGAAC CCAGGTGAGG TTACAGCCAT GTCTGAAATC  
10701 ACCACGAACA GACTGACAGC TACTCAATCA ACAGCACCCA AAGGGATACC  
10751 TGTGAAGCCC ACCAGTGCTG AGTCAGGCCT CCTAACACCT GTCTCTGCCT  
10801 CCTCAAGCCC ATCAAAGGCC TTTGCCTCAC TGA CTACAGC TCCCCAACT  
10851 TGGGGGATCC CACAGTCTAC CTTGACATT GAGTTTCTG AGGTCCCAAG  
10901 TTTGGATACT AAGTCCGCTT CTTTACCAAC TCCTGGACAG TCCCTGAACA

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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10951 CCATTCCAGA CTCAGATGCA AGCACAGCAT CTCCTCACT GTCCAAGTCT  
 11001 CCAGAAAAAA ACCCAAGGGC AAGGATGATG ACTTCCACAA AGGCCATAAG  
 11051 TGCAAGCTCA TTTCAATCAA CAGGTTTTAC TGAAACCCCT GAGGGATCTG  
 11101 CCTCCCCTTC TATGGCAGGG CATGAACCCA GAGTCCCAC TTCAGGAACA  
 11151 GGGGACCCTA GATATGCCTC AGAGAGCATG TCTTATCCAG ACCCAAGCAA  
 11201 GGCATCATCA GCTATGACAT CGACCTCTCT TGCATCAAAA CTCACAATC  
 11251 TCTTCAGCAC AGGTCAAGCA GCAAGGTCTG GTTCTAGTTC CTCTCCATA  
 11301 AGCCTATCCA CTGAGAAAGA AACAAGCTTC CTTTCCCCCA CTGCATCCAC  
 11351 CTCCAGAAAG ACTTCACTAT TTCTTGGGCC TTCCATGGCA AGGCAGCCCA

[0054] 11401 ACATATTGGT GCATCTTCAG ACTTCAGCTC TGACACTTTC  
 TCCAACATCC

11451 ACTCTAAATA TGTCCCAGGA GGAGCCTCCT GAGTTAACCT CAAGCCAGAC  
 11501 CATTGCAGAA GAAGAGGGAA CAACAGCTGA AACACAGACG TTAACCTTCA  
 11551 CACCATCTGA GACCCCAACA TCCTTGTTAC CTGTCTCTTC TCCCACAGAA  
 11601 CCCACAGCCA GAAGAAAGAG TTCTCCAGAA ACATGGGCAA GCTCTATTTT  
 11651 AGTTCCTGCC AAGACCTCCT TGGTTGAAAG TAAGAATGCC CTGCTCCTTC  
 11701 CCCAAGTGTG CTGGGGATGA ATCTGGAAAT AACTACATC TTTTTTATTT  
 11751 TTTAAACTTT TATATTTGAA AATATAAATA TTTTAGGTTC AGGGAACATG  
 11801 TGCAGGTTTG TTATATAGGT AAATTGCATG TCATGGGGGC TTGGGGTACA  
 11851 GATTACATCA TCAGCCAGGT AATAAGCCTA GTACCTGATC AGTAGATTTT  
 11901 TTTTAATCCT CTCCCTCCTC CCAGCCTCCA CCCTCAATTC ACATGTCTCC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
11951	ATGTGTACTC	AAGGTTTAAT	TCCCACTTAT	GAGTGAGAAC	ATGCGGTATT
12001	TGTAAACTAC	ATCTTTATTT	TTGCTAACCT	CGAACTGAAA	TTTAGCATTT
12051	GTTTTATTGA	TGAATAGAGG	TAACAAAACA	AACCACATTA	ATCCTAGCAG
12101	TGCCTGTGCC	TTTGCCAACA	ACAGAAATTC	CGGACACTTT	CATATCCTAT
12151	GACAATTGTT	GCAAGCACTT	TTAAAAATCA	TGTACGACTT	TATTCATAAT
12201	TATAGTGGTT	ATTAGGCTTT	TCAATAGATC	TTATTTAATG	AGTTAGTAAA
12251	ATAAGTGCCT	GTATTATTGT	ATTACATTTG	TTTATTAAGA	TCTTGATAAC
12301	AACATTTCAA	TATAATCATT	TCCTTTGTTT	TTTAAATTTT	AGATTCAGGG
12351	GTATATGTGC	AGGTTTGTTA	CGTGGATATA	CTGCATAATG	ATGAGGTTTG
12401	GCTTCTAGTG	AACCCATCAG	CCAAATAGTG	AATGTTGTGC	CCAATAAGTA
12451	GTTTTTCAAT	CCTCACTTCA	CTCCCAGCCT	CCTCTATTTT	GGAGTCCCAG
12501	TGTCTATTAT	TTCTATCTTT	ATGTCCACAT	GTACCCATTG	GTTAGCTCCC
12551	ACTTATAAGT	GAGAATGTGC	AGTATTTAAT	TTTCTGTTTT	TGAGTTATTT
12601	TGCTTAGGTT	GATGGCCTTC	AGCTCCAGCC	ACGTTGCTTT	AAAGAACATG
12651	ATTTCAATTCT	TTTTTATGGC	TGCATAGTAC	TCCGAGGTGT	ATGTGTACCA
12701	GATTTTCTTT	ATCCACAATG	ATTCCTTTG	TAATCTAATA	TTTTATATTG
12751	TTATTTTATG	TTTTATTCTA	TATTTTATT	TTAATTTATA	AAGGAATTCA
12801	TATGGTTCAC	AAGCCTGTCA	AAGGGACCTA	TAATAAAAAG	AGGTTAAGAA
12851	TCCATGCTCT	AAACAGAATA	TTACTCCATT	TTATTTTCATT	TATTTTTTAA
12901	GAGACAGTCT	CACTCTGTCA	TCCAGGCTGG	AGTACAGTGG	AGTGATCATA

Table 1 (continued)

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**Genomic CA125 Amino Terminal Sequence**  
(SEQ ID NO: 1)

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12951 GCTCATTGCA ACCCTGAACT CTTGGGCACA AGCAATTCTC CTGCTTCATC  
 13001 CTCCAGAGGA GCTGGGACTA CAGGTGCACA TCACCATGCC CAGCTAGTTT  
 13051 TAAAAATTAT TTTGTAGAGA TGGTGTCTCA CTATCCTACC CAGGCTGGTC  
 13101 TCAAATCCT GGGCTCAGGC AATCCTCCCA CTTTGACCTC CCAAAGTGTT  
 13151 GAGATTACAG GGGCAAGCCA CTGTGCCTGG CCACTTGTC AATTTTAATT  
 13201 TGTGATTACT TATAAAATGA ACCCCTTCCC ATCTGAGATC TGTCAGTCTT  
 13251 TCTGGTQACG GTGCCTGGTG TCTGCTTTCT ACCATGTCCT GTTAGACTAG  
 13301 TGTTTGATGG GAGGTCACCT GGGCAGCTGT CCAGCTCACT CACTGGGCTC  
 13351 TAGAGCCTCT GAGTTGAAGC AAAATAGAAA GATCAGTCAA TGTAAGAAA  
 13401 GCTCAAAAAC TGACATTCTG AAGTAATGGA TAGCTAAACC TTCCTATTGC

**Exon 2**

13451 CCTTTTCTTT CAGCAACTGA TGGAACGCTA GTGACCACCA TAAAGATGTC  
 13501 AAGCCAGGCA GCACAAGGAA ATTCCACGTG GCCTGCCCCA GCAGAGGAGA  
 13551 CGGGGACCAG TCCAGCAGGT AAATATAGAC CTTGTTTCCA TTTCTGCTCT  
 13601 GCTAATGCCA CCCAAGCCTT TCTTTTCTTT TCTTTTCTTT TCTTTTCTTT  
 13651 TCTTTTCTTT TCTTTTCTTT CTCTCCCTTT CTTTCTTTCT TTCTTTCTTT  
 13701 CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT CTTTCTTTCT TTCTTTCTTT  
 13751 CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT CTTTCTTTCT TCTTTCTCTC  
 13801 TCTCTCTTTC TTTCTTTCTC TTGTTCTTTT TAAATTTTTT ATTTTTTTAC  
 13851 TTAATTTTTT TCACCCAAGC CTTAAGGCCA GTTTGGACCA GATAGTGAGA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
13901	CCCCACCTCT	ATAAAAAAAAA	TTTTTAAAAA	AAAAATAAGT	TGGGCATCGT
13951	GCAGGCCTGT	AGTCCCTGCT	ACTCGAGAGG	CCAAGGTGGG	AGGACAGCTT
14001	GCTGCTGACT	AAAAGTGCTG	CTTATTGATT	CTGGGAAGAA	AAAATATACA
14051	AGGCTTCAGT	TTCATTATTT	TATAAGTAAA	TGCTAGCAAC	TTTTCCTTTC
14101	TTTCTCTCTT	TCTCTCTTCC	TCTCTTTCTC	TCCTCTCCTT	CTCTTCTCTC
14151	TCTCTCTCTC	TCTCTCTCTC	TTTCTCTCTC	CTCTCCTTCT	CTTCTCTTCT
14201	TTCTCTCTCT	CTCTCTTTCA	TTTATTTTGT	AGACATGGTC	TCATTCTGTC
14251	ACCCAGGCTG	GAGTACAGTG	GTGTATATTT	ACTGCAGTAC	TCACTGTACT
14301	CACTGCAGCC	TCAAATTCCT	GGGCTCAAGC	TATCCTCTCA	CCTCAGCCTC
14351	CTGAGTAGCT	GGGCAGCAGT	CCAGCTCACT	CACTGGGCTC	TAGAGCCTCT
14401	GTGCTATGCC	CAGCTTATTG	TTGTTGTTTT	TTTAAATTTT	TTTTTTTGTA
14451	CAGATGGGGT	CTCACTATGT	GGCCCAAGGT	GGTCTTAAAC	TCCTGGCTCC
14501	AAGAGATCCT	CCCACCTCAG	CCTCCCAAAG	TGCAGGGATT	ACAGGTGTGA
14551	GCCACTGTGC	CCAGCCTAGA	CAGCATTTTT	TTTTTTTGAA	ACAGGGTCTC
14601	CCTCTGTTGC	CCAGGCTGGA	GTGCAATGGC	GTGTTTATGG	TTCCTGCAG
14651	CCTCAGCCTC	CTCAGTCTCA	AGCAATCCTC	CAACTTCAGC	CTCCCCAAC
14701	AGCTAGAACT	GCAGGTGATC	ATCACCAATT	AGCCTGGTTA	ATTGTGTGTG
14751	TATTTCTTAA	ATTTTTTGTA	GAGATAGTTC	TCACTATATT	GCTTGGGCTG
14801	GTCTCAAAC	CCTGGACTCA	AGTGATTCAC	CTACCTCGGC	CTCCCTAAGC
14851	ACTGGGATTA	CAGGCTTGAG	CCACCACACC	CGGCAAGGAC	TAGGTTTTAA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
14901	AATAGGTTCC TAGGCTGGGT GTGGTGGCTT ACGCCCGTAA TCCCAGCACT
14951	TTGGGAGGCT GAGGTGGGCG GATCACGAGG TCAGGAGTTT GAGACCAGCC
15001	TGGCCAACAT AGTGAAACCC TGTCTCTACT AAAAATACAA AAAATTAGCT
15051	GGGCATAGTG GCACACACCT GTAATCCCAG CTACTCGGGA GGCTGAGGAA
15101	GGAGAATCAC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCAT
15151	GCCATTGCTC TCCAGCCTGG GTGACAGAGC AAGACTCCAT CTAAAAA
15201	AAAAAAAAGT TCCTTTGACT TCTTGACACT CTTCTCTGAG GATATTGATC
15251	ATTTTCCCC AATAGATGTT ACTAATTGAA CACTTCTGTT GCTTCAACTT
15301	ACTAATTTAC ATGATCAATA GCCAATTAAT TCAGCAGGAG AGAATGCTAC
15351	AGAGTCGATT CTTTCTGTAC TTTCTTCTGC TCCAGAGTGA AGGATCTTTC
15401	TAAATCAGAG ACCATCACTG TGTTACACAGG GAGGGCCTAG GTGAACCTGA
15451	GATGGCAAAT GTTGCGTTTG TTCTACGGAA GAAGGGATTA TGGGTTGAAG
15501	TCCTTGGCAG TGCCAAATTG CTTAGAAAAA TGTGAAATAT GGTCCCTAGG
15551	AGTGCTCTTG GGATGTCACA TTTTCTCAC TCCTTTGACA GGTAGATGTT
15601	ATTTTCTTGA AGGCCAGGGA AAGGATTCAG AGGGAGGAAT GAATTTGAAA
15651	GAAAATGAAG GTGACGAGAA AGAATGAGCT CATCTCCCTT ATCCTCTTTC
15701	TTCTCAAATC CTTAAGTAGC TTTGCAGTGA ACTAAGATTT GGGGGAACCT
15751	AGAGGAGGCT GAAAGTTGGA AGCTGAAATT GGCTTAGCAA GGGCAAGCTC
15801	CAAAGACAAA AGTGGAATA GTTTGGGGGT AGCCTTTTGC ATGGGTGAAA
15851	TCCTGGTTCA TCACATCCTC CTTATGCAA AGAGCCCTTT TATATGGGGC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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15901 ATGGGGAAAA ACTGAGCTAA AGGTGATAAT TTCTCCTGAG CAAGCCAGAT  
 15951 GGTCAAAGCT CTAACCTCAC CATCTCCCTT GGAATGTTTA ATGTGTTCCC  
 16001 TGGTGTCCAG AGGCTTAACG TGTGAGAATT AAAAGCTCAA CATTCTCTTT  
 16051 CCCAGGGAAG GAGGAAATAG TTTTAATTGA AATCCCGGGA GGAAATGAAT  
 16101 GATAGTGTCA AACCAAAAAA CTTCATCTTC TGTACCACTT GCATATACTC

**Exon 3**

16151 CACTGACTTA CTTTCTAATC ACAGGCACAT CCCCAGGAAG CCCAGAAATG  
 16201 TCTACCACTC TCAAAATCAT GAGCTCCAAG GAACCCGGCA TCAGCCCAGA  
 16251 GATCAGGTCC ACTGTGAGAA ATTCTCCTTG GAAGACTCCA GAAACAAC TG  
 16301 TTCCCATGGA GACCACAGTG GAACCACTCA CCCTTCAGTC CACAGCCCTA  
 16351 GGAAGTGGCA GCACCAGCAT CTCTCACCTG CCCACAGGAA CCACATCACC  
 16401 AACCAAGTCA CCAACAGAAA ATATGTTGGC TACAGAAAGG GTCTCCCTCT  
 16451 CCCCATCCCC ACCTGAGGCT TGGACCAACC TTTATTCTGG AACTCCAGGA  
 16501 GGGACCAGGC AGTCACTGGC CACAATGTCC TCTGTCTCCC TAGAGTCACC  
 16551 AACTGCTAGA AGCATCACAG GGAAGGTCA GCAAAGCAGT CCAGAACTGG  
 16601 TTTTAAAGAC AACTGGAATG GAATTCTCTA TGTGGCATGG CTCTACTGGA  
 16651 GGGACCACAG GGGACACACA TGTCTCTCTG AGCACATCTT CCAATATCCT  
 16701 TGAAGACCCT GTAACCAGCC CAACTCTGT GAGCTCAT TG ACAGATAAAT  
 16751 CCAAACATAA AACCGAGACA TGGGTCAGCA CCACAGCCAT TCCCTCCACT  
 16801 GTCCTGAATA ATAAGATAAT GGCAGCTGAA CAACAGACAA GTCGATCTGT

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
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16851	<u>GGATGAGGCT TATTCATCAA CTAGTTCCTG GTCAGATCAG ACATCTGGGA</u>
16901	<u>GTGACATCAC CCTTGGTGCA TCTCCTGATG TCACAAACAC ATTATACATC</u>
16951	<u>ACCTCCACAG CACAAACCAC CTCACTAGTA TCTCTGCCCT CTGGAGACCA</u>
17001	<u>AGGCATTACA AGCCTCACCA ATCCCTCAGG AGGAAAAACA AGCTCTGCAT</u>
17051	<u>CATCTGTCAC ATCTCCTTCA ATAGGGCTTG AGACTCTGAT GGCCAATGTA</u>
17101	<u>AGTGCAGTGA CAAGTGACAT TGCCCCTACT GCTGGGCATC TATCTCAGAC</u>
17151	<u>TTCATCTCCT GCGGAAGTGA GCATCCTGGA CATAACCACA GCTCCTACTC</u>
17201	<u>CAGGTATCTC CACCACCATC ACCACCATGG GAACCAACTC AATCTCAACT</u>
17251	<u>ACCACACCCA ACCCAGAAGT GGGTATGAGT ACCATGGACA GCACCCCGGC</u>
17301	<u>CACAGAGAGG CACACAACTT CTACAGAACA CCCTTCCACC TGGTCTTCCA</u>
17351	<u>CAGCTGCATC AGATTCTGCTG ACTGTCACAG ACATGACTTC AAACTTGAAA</u>
17401	<u>GTTGCAAGAT CTCCTGGAAC AATTTCACCA ATGCATACAA CTTCATTCTT</u>
17451	<u>AGCCTCAAGC ACTGAATTAG ACTCCATGTC TACTCCCCAT GGCCGTATAA</u>
17501	<u>CTGTCATTGG AACCAGCCTG GTCACTCCAT CCTCTGATGC TTCAGCTGTA</u>
17551	<u>AAGACAGAGA CCAGTACAAG TGAAAGAACA TTGAGTCCTT CAGACACAAC</u>
17601	<u>TGCATCTACT CCCATCTCAA CTTTTTCTCG TGTCCAGAGG ATGAGCATCT</u>
17651	<u>CAGTTCCTGA CATTTTAAGT ACAAGTTGGA CTCCCAGTAG TACAGAAGCA</u>
17701	<u>GAAGATGTGC CTGTTTCAAT GGTTCCTACA GATCATGCTA GTACAAAGAC</u>
17751	<u>TGACCCAAAT ATGCCCTGT CCACTTTTCT GTTTGATTCT CTGTCCACTC</u>
17801	<u>TTGACTGGGA CACTGGGAGA TCTCTGTCAT CAGCCACAGC CACTACCTCA</u>



Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
17851	<u>GCTCCTCAGG GGGCCACAAC TCCCCAAGAA CTCACTTTGG AAACCATGAT</u>
17901	<u>CAGCCCAGCT ACCTCACAGT TGCCCTTCTC TATAGGGCAC ATTACAAGTG</u>
17951	<u>CAGTCATACC AGCTGCAATG GCAAGGAGCT CTGGAGTTAC TTTTCAAGA</u>
18001	<u>CCAGATCCCA CAAGCAAAAA GGCAGAGCAG ACTTCCACTC AGCTTCCCAC</u>
18051	<u>CACCACTTCT GCACATCCAG AGCAGGTGCC CAGATCAGCA GCAACAATC</u>
18101	<u>TGGATGTGAT CCCACACACA GCAAAAACTC CAGATGCAAC TTTTCAGAGA</u>
18151	<u>CAAGGGCAGA CAGCTCTTAC AACAGAGGCA AGAGCTACAT CTGACTCCTG</u>
18201	<u>GAATGAGAAA GAAAAATCAA CCCCAAGTGC ACCTTGGATC ACTGAGATGA</u>
18251	<u>TGAATTCTGT CTCAGAAGAT ACCATCAAGG AGGTACCAG CTCCTCCAGT</u>
18301	<u>GTGTTAAGGA CCCTGAATAC GCTGGACATA AACTTGGAAT CTGGGACGAC</u>
18351	<u>TCATCCCCA AGTTGGAAAA GCAGCCCATA TGAGAGAATT GCCCCTTCTG</u>
18401	<u>AGTCTACCAC AGACAAAGAG GCAATTCACC ( TCTAC/AA CACAGTAGAG</u>
18451	<u>ACCACTGGCT GGGTCACAAG TTCCGAACAT GCTTCTCATT CCACTATCCC</u>
18501	<u>AGCCCACTCA GCGTCATCCA AACTCACATC TCCAGTGGTT ACAACCTCCA</u>
18551	<u>CCAGGGAACA AGCAATAGTT TCTATGTCAA CAACCACATG GCCAGAGTCT</u>
18601	<u>ACAAGGGCTA GAACAGAGCC TAATTCCTTC TTGACTATTG AACTGAGGGA</u>
18651	<u>CGTCAGCCCT TACATGGACA CCAGCTCAAC CACACAAACA AGTTTTATCT</u>
18701	<u>CTTCCCCAGG TTCCACTGCG ATCACCAAGG GGCCTAGAAC AGAAATTACC</u>
18751	<u>TCCTCTAAGA GAATATCCAG CTCATTCCTT GCCCAGTCTA TGAGGTCGTC</u>
18801	<u>AGACAGCCCC TCAGAAGCCA TCTCCAGGCT GTCTAACTTT CCTGCCATGA</u>

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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18851 CAGAATCTGG AGGAATGATC CTTGCTATGC AAACAAGTCC ACCTGGCGCT

18901 ACATCACTAA GTGCACCTAC TTTGGATACA TCAGCCACAG CCTCCTGGAC

18951 AGGGACTCCA CTGGCTACGA CTCAGAGATT TACATACTCA GAGAAGACCA

19001 CTCTCTTTAG CAAAGGTCCT GAGGATACAT CACAGCCAAG CCCTCCCTCT

19051 GTGGAAGAAA CCAGCTCTTC CTCTTCCCTG GTACCTATCA ATGCTACAAC

19101 CTCGCCTTCC AATATTTTGT TGACATCACA AGGGCACAGT CCCTCCTCTA

19151 CTCCACCTGT GACCTCAGTT TTCTTGTCTG AGACCTCTGG CCTGGGGAAG

19201 ACCACAGACA TGTCGAGGAT AAGCTTGGA CCTGGCACAA GTTTACCTCC

19251 CAATTTGAGC AGTACAGCAG GTGAGGCGTT ATCCACTTAT GAAGCCTCCA

19301 GAGATACAAA GGCAATTCAT CATTCTGCAG ACACAGCAGT GACGAATATG

19351 GAGGCAACCA GTTCTGAATA TTCTCCTATC CCAGGCCATA CAAAGCCATC

19401 CAAAGCCACA TCTCCATTGG TTACCTCCCA CATCATGGGG GACATCACTT

19451 CTTCCACATC AGTATTTGGC TCCTCCGAGA CCACAGAGAT TGAGACAGTG

19501 TCCTCTGTGA ACCAGGGACT TCAGGAGAGA AGCACATCCC AGGTGGCCAG

19551 CTCTGCTACA GAGACAAGCA CTGTCATTAC CCATGTGTCT AGTGGTGATG

19601 CTACTACTCA TGTCACCAAG ACACAAGCCA CTTTCTCTAG CGGAACATCC

19651 ATCTCAAGCC CTCATCAGTT TATAACTTCT ACCAACACAT TTACAGATGT

19701 GAGCACCAAC CCCTCCACCT CTCTGATAAT GACAGAATCT TCAGGAGTGA

19751 CCATCACCAC CCAAACAGGT CCTACTGGAG CTGCAACACA GGGTCCATAT

19801 CTCTTGGA CAATCAACCAT GCCTTACTTG ACAGAGACTC CATTAGCTGT

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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19851 GACTCCAGAT TTTATGCAAT CAGAGAAGAC CACTCTCATA AGCAAAGGTC  
19901 CCAAGGATGT GTCCTGGACA AGCCCTCCCT CTGTGGCAGA AACCAGCTAT  
19951 CCCTCTTCCC TGACACCTTT CTTGGTCACA ACCATACCTC CTGCCACTTC  
20001 CACGTTACAA GGGCAACATA CATCCTCTCC TGTTTCTGCG ACTTCAGTTC  
20051 TTACCTCTGG ACTGGTGAAG ACCACAGATA TGTTGAACAC AAGCATGGAA  
20101 CCTGTGACCA ATTCACCTCA AAATTGAAAC AATCCATCAA ATGAGATACT  
20151 GGCCACTTTG GCAGCCACCA CAGATATAGA GACTATTCAT CCTTCCATAA  
20201 ACAAAGCAGT GACCAATATG GGGACTGCCA GTTCAGCACA TGTACTGCAT  
20251 TCCACTCTCC CAGTCAGCTC AGAACCATCT ACAGCCACAT CTCCAATGGT  
20301 TCCTGCCTCC AGCATGGGGG ACGCTCTTGC TTCTATATCA ATACCTGGTT  
20351 CTGAGACCAC AGACATTGAG GGAGAGCCAA CATCCTCCCT GACTGCTGGA  
20401 CGAAAAGAGA ACAGCACCT CCAGGAGATG AACTCAACTA CAGAGTCAAA  
20451 CATCATCCTC TCCAATGTGT CTGTGGGGGC TATTACTGAA GCCACAAAAA  
20501 TGGAAGTCCC CTCTTTTGAT GCAACATTCA TACCAACTCC TGCTCAGTCA  
20551 ACAAAGTTCC CAGATATTTT CTCAGTAGCC AGCAGTAGAC TTTCAAACCTC  
20601 TCCTCCCATG ACAATATCTA CCCACATGAC CACCACCCAG ACAGGGTCTT  
20651 CTGGAGCTAC ATCAAAGATT CCACTTGCCT TAGACACATC AACCTTGGA  
20701 ACCTCAGCAG GGA CTCCATC AGTGGTGACT GAGGGGTTTG CCCACTCAA  
20751 AATAACCACT GCAATGAACA ATGATGTCAA GGACGTGTCA CAGACAAACC  
20801 CTCCCTTTCA GGATGAAGCC AGCTCTCCCT CTTCTCAAGC ACCTGTCCTT

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
<hr/>	
20851	<u>GTCACAACCT TACCTTCTTC TGTTGCTTTC ACACCGCAAT GGCACAGTAC</u>
20901	<u>CTCCTCTCCT GTTCTATGT CCTCAGTTCT TACTTCTTCA CTGGTAAAGA</u>
20951	<u>CCGCAGGCAA GGTGGATACA AGCTTAGAAA CAGTGACCAG TTCACCTCAA</u>
21051	<u>AGATATAGAG ACAACGCATC CTTCATAAA CACAGTAGTT ACCAATGTGG</u>
21101	<u>GGACCACCGG TTCAGCATTT GAATCACATT CTACTGTCTC AGCTTACCCA</u>
21151	<u>GAGCCATCTA AAGTCACATC TCCAAATGTT ACCACCTCCA CCATGGAAGA</u>
21201	<u>CACCACAATT TCCAGATCAA TACCTAAATC CTCTAAGACT ACAAGAACTG</u>
21251	<u>AGACTGAGAC AACTTCCTCC CTGACTCCTA AACTGAGGGA GACCAGCGTC</u>
21301	<u>TCCCAGGAGA TCACCTCGTC CACAGAGACA AGCACTGTTC CTTACAAAGA</u>
21351	<u>GCTCACTGGT GCCACTACCG AGGTATCCAG GACAGATGTC ACTTCCTCTA</u>
21401	<u>GCAGTACATC CTTCCCTGGC CCTGATCAGT CCACAGTGTC ACTAGACATC</u>
21451	<u>TCCACAGAAA CCAACACCAG GCTGTCTACC TCCCCAATAA TGACAGAATC</u>
21501	<u>TGCAGAAATA ACCATCACCA CCCAAACAGG TCCTCATGGG GCTACATCAC</u>
21551	<u>AGGATACTTT TACCATGGAC CCATCAAATA CAACCCCCCA GGCAGGGATC</u>
21601	<u>CACTCAGCTA TGA CT CATGG ATTTTCACAA TTGGATGTGA CCACTCTTAT</u>
21651	<u>GAGCAGAATT CCACAGGATG TATCATGGAC AAGTCCTCCC TCTGTGGATA</u>
21701	<u>AAACCAGCTC CCCCTCTTCC TTTCTGCCCT CACCTGCAAT GACCACACCT</u>
21751	<u>TCCCTGATTT CTTCTACCTT ACCAGAGGAT AAGCTCTCCT CTCCTATGAC</u>
21801	<u>TTCACTTCTC ACCTCTGGCC TAGTGAAGAT TACAGACATA TTACGTACAC</u>
21851	<u>GCTTGGAACC TGTGACCAGC TCACTTCCAA ATTTCAGCAG CACCTCAGAT</u>

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Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
21901	<u>AAGATACTGG CCACTTCTAA AGACAGTAAA GACACAAAGG AAATTTTTC</u>
21951	<u>TTCTATAAAC ACAGAAGAGA CCAATGTGAA AGCCAACAAC TCTGGACATG</u>
22001	<u>AATCCCATTG CCTGCACTG GCTGACTCAG AGACACCCAA AGCCACAAC</u>
22051	<u>CAAATGGTTA TCACCACCAC TGTGGGAGAT CCAGCTCCTT CCACATCAAT</u>
22101	<u>GCCAGTGCAT GGTTCCTCTG AGACTACAAA CATTAAGAGA GAGCCAACAT</u>
22151	<u>ATTTCTTGAC TCCTAGACTG AGAGAGACCA GTACCTCTCA GGAGTCCAGC</u>
22201	<u>TTTCCCACGG ACACAAGTTT TCTACTTTCC AAAGTCCCCA CTGGTACTAT</u>
22251	<u>TACTGAGGTC TCCAGTACAG GGGTCATCTC TTCTAGCAA ATTTCCACCC</u>
22301	<u>CAGACCATGA TAAGTCCACA GTGCCACCTG ACACCTTCAC AGGAGAGATC</u>
22351	<u>CCCAGGGTCT TCACCTCCTC TATTAAGACA AAATCTGCAG AAATGACGAT</u>
22401	<u>CACCACCCAA GCAAGTCCTC CTGAGTCTGC ATCGCACAGT ACCCTTCCCT</u>
22451	<u>TGGACACATC AACCACACTT TCCCAGGGAG GGACTCATTC AACTGTGACT</u>
22501	<u>CAGGGATTCC CATACTCAGA GGTGACCACT CTCATGGGCA TGGGTCCTGG</u>
22551	<u>GAATGTGTCA TGGATGACAA CTCCCCCTGT GGAAGAAACC AGCTCTGTGT</u>
22601	<u>CTTCCCTGAT GTCTTCACCT GCCATGACAT CCCCTTCTCC TGTTCCTCC</u>
22651	<u>ACATCACCAC AGAGCATCCC CTCCTCTCCT CTTCTGTGA CTGCACTTCC</u>
22701	<u>TACTTCTGTT CTGGTGACAA CCACAGATGT GTTGGGCACA ACAAGCCCAG</u>
22751	<u>AGTCTGTAAC CAGTTCACCT CCAAATTGA GCAGCATCAC TCATGAGAGA</u>
22801	<u>CCGGCCACTT ACAAAGACAC TGCACACACA GAAGCCGCCA TGCATCATTC</u>
22851	<u>CACAAACACC GCAGTGACCA ATGTAGGGAC TTCCGGGTCT GGACATAAAT</u>

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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22901 CACAATCCTC TGTCTAGCT GACTCAGAGA CATCGAAAGC CACACCTCTG  
22951 ATGAGTACCA CCTCCACCCT GGGGGACACA AGTGTTTCCA CATCAACTCC  
23001 TAATATCTCT CAGACTAACC AAATTCAAAC AGAGCCAACA GCATCCCCTGA  
23051 GCCCTAGACT GAGGGAGAGC AGCACGTCTG AGAAGACCAG CTCAACAACA  
23101 GAGACAAATA CTGCCTTTTC TTATGTGCCC ACAGGTGCTA TTA CT CAGGC  
23151 CTCCAGAACA GAAATCTCCT CTAGCAGAAC ATCCATCTCA GACCTTGATC  
23201 GGTCCACAAT AGCACCCGAC ATCTCCACAG GAATGATCAC CAGGCTCTTC  
23251 ACCTCCCCCA TCATGACAAA ATCTGCAGAA ATGACCGTCA CCACTCAAAC  
23301 AACTACTCCT GGGGCTACAT CACAGGGTAT CCTTCCCTGG GACACATCAA  
23351 CCACACTTTT CCAGGGAGGG ACTCATTCAA CCGTGTCTCA GGGATTCCCA  
23401 CACTCAGAGA TAACCACTCT TCGGAGCAGA ACCCCTGGAG ATGTGTCATG  
23451 GATGACAACT CCCCCTGTGG AAGAAACCAG CTCTGGGTTT TCCCTGATGT  
23501 CACCTTCCAT GACATCCCCT TCTCCTGTTT CCTCCACATC ACCAGAGAGC  
23551 ATCCCCTCCT CTCCTCTCCC TGTGACTGCA CTTCTTACTT CTGTTCTGGT  
23601 GACAACCACA AATGTATTGG GCACAACAAG CCCAGAGCCC GTAACGAGTT  
23651 CACCTCCAAA TTAAGCAGC CCCACACAGG AGAGACTGAC CACTTACAAA  
23701 GACACTGCGC ACACAGAAGC CATGCATGCT TCCATGCATA CAAACACTGC  
23751 AGTGGCCAAC GTGGGGACCT CCATTTCTGG ACATGAATCA CAATCTTCTG  
23801 TCCCAGCTGA TTCAGACACA TCAAAGCCA CATCTCCAAT GGGTACCACC  
23851 TTCGCCATGG GGGATACAAG TGTTTCTACA TCAACTCCTG CCTTCTTTGA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
23901	<u>GACTAGAATT CAGACTGAAT CAACATCCTC TTTGATTCTT GGATTAAGGG</u>
23951	<u>ACACCAGGAC GTCTGAGGAG ATCAACACTG TGACAGAGAC CAGCACTGTC</u>
24001	<u>CTTTCAGAAG TGCCCACTAC TACTACTACT GAGGTCTCCA GGACAGAAGT</u>
24051	<u>TATCACTTCC AGCAGAACAA CCATCTCAGG GCCTGATCAT TCCAAAATGT</u>
24101	<u>CACCCTACAT CTCCACAGAA ACCATCACCA GGCTCTCCAC TTTTCCTTTT</u>
24151	<u>GTAACAGGAT CCACAGAAAT GGCCATCACC AACCAAACAG GTCCTATAGG</u>
24201	<u>GACTATCTCA CAGGCTACCC TTACCCTGGA CACATCAAGC ACAGCTTCCT</u>
24251	<u>GGGAAGGGAC TCACTCACCT GTGACTCAGA GATTTCACA CTCAGAGGAG</u>
24301	<u>ACCACTACTA TGAGCAGAAG TACTAAGGGC GTGTCATGGC AAAGCCCTCC</u>
24351	<u>CTCTGTGGAA GAAACCAGTT CTCCTTCTTC CCCAGTGCCT TTACCTGCAA</u>
24401	<u>TAACCTCACA TTCATCTCTT TATTCCGAG TATCAGGAAG TAGCCCCACT</u>
24451	<u>TCTGCTCTCC CTGTGACTTC CTTTCTCACC TCTGGCAGGA GGAAGACCAT</u>
24501	<u>AGACATGTTG GACACACACT CAGAACTTGT GACCAGCTCC TTACCAAGTG</u>
24551	<u>CAAGTAGCTT CTCAGGTGAG ATACTCACTT CTGAAGCCTC CACAAATACA</u>
24601	<u>GAGACAATTC ACTTTTCAGA GAACACAGCA GAAACCAATA TGGGGACCAC</u>
24651	<u>CAATTCTATG CATAAACTAC ATTCTCTGT CTCAATCCAC TCCCAGCCAT</u>
24701	<u>CCGGACACAC ACCTCCAAAG GTTACTGGAT CTATGATGGA GGACGCTATT</u>
24751	<u>GTTTCCACAT CAACACCTGG TTCTCCTGAG ACTAAAAATG TTGACAGAGA</u>
24801	<u>CTCAACATCC CCTCTGACTC CTGAACTGAA AGAGGACAGC ACCGCCCTGG</u>
24851	<u>TGATGAACTC AACTACAGAG TCAAACACTG TTTTCTCCAG TGTGTCCCTG</u>

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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24901 GATGCTGCTA CTGAGGTCTC CAGGGCAGAA GTCACCTACT ATGATCCTAC

24951 ATTCATGCCA GCTTCTGCTC AGTCAACAAA GTCCCCAGAC ATTTACCTG

25001 AAGCCAGCAG CAGTCATTCT AACTCTCCTC CCTTGACAAT ATCTACACAC

25051 AAGACCATCG CCACACAAAC AGGTCTTCTT GGGGTGACAT CTCTTGGCCA

25101 ACTGACCCTG GACACATCAA CCATAGCCAC CTCAGCAGGA ACTCCATCAG

25151 CCAGAACTCA GGATTTTGTA GATTCAGAAA CAACCAGTGT CATGAACAAT

25201 GATCTCAATG ATGTGTTGAA GACAAGCCCT TTCTCTGCAG AAGAAGCCAA

25251 CTCTCTCTCT TCTCAGGCAC CTCTCCTTGT GACAACCTCA CCTTCTCCTG

25301 TAACTTCCAC ATTGCAAGAG CACAGTACCT CCTCTCTTGT TTCTGTGACC

25351 TCAGTACCCA CCCCTACACT GCGAAGATC ACAGACATGG ACACAAACTT

25401 AGAACCTGTG ACTCGTTCAC CTCAAATTT AAGGAACACC TTGGCCACTT

25451 CAGAAGCCAC CACAGATACA CACACAATGC ATCCTTCTAT AAACACAGCA

25501 GTGGCCAATG TGGGGACCAC CAGTTCACCA AATGAATTCT ATTTTACTGT

25551 CTCACCTGAC TCAGACCCAT ATAAAGCCAC ATCCGCAGTA GTTATCACTT

25601 CCACCTCGGG GGACTCAATA GTTCCACAT CAATGCCTAG ATCCTCTGCG

25651 ATGAAAAAGA TTGAGTCTGA GACAACTTTC TCCCTGATAT TTAGACTGAG

25701 GGAGACTAGC ACCTCCCAGA AAATTGGCTC ATCCTCAGAC ACAAGCACGG

25751 TCTTTGACAA AGCATTCACT GCTGCTACTA CTGAGGTCTC CAGAACAGAA

25801 CTCACCTCCT CTAGCAGAAC ATCCATCCAA GGCCTGAAA AGCCCACAAT

25851 GTCACCGGAC ACCTCCACAA GATCTGTCAC CATGCTTTCT ACTTTTGCTG



Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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25901 GCCTGACAAA ATCCGAAGAA AGGACCATTG CCACCCAAAC AGGTCCTCAT  
25951 AGGGCGACAT CACAGGGTAC CCTTACCTGG GACACATCAA TCACAACCTC  
26001 ACAGGCAGGG ACCCACTCAG CTATGACTCA TGGATTTTCA CAATTAGATT  
26051 TGTCCACTCT TACGAGTAGA GTTCCTGAGT ACATATCAGG GACAAGCCCA  
26101 CCCTCTGTGG AAAAAACCAG CTCTTCCTCT TCCCTTCTGT CTTTACCAGC  
26151 AATAACCTCA CCGTCCCCTG TACCTACTAC ATTACCAGAA AGTAGGCCGT  
26201 CTTCTCCTGT TCATCTGACT TCACTCCCCA CCTCTGGCCT AGTGAAGACC  
26251 ACAGATATGC TGGCATCTGT GGCCAGTTTA CCTCCAAACT TGGGCAGCAC  
26301 CTCACATAAG ATACCGACTA CTTCAGAAGA CATTAAAGAT ACAGAGAAAA  
26351 TGTATCCTTC CACAAACATA GCAGTAACCA ATGTGGGGAC CACCACTTCT  
26401 GAAAAGGAAT CTTATTCGTC TGTCCCAGCC TACTCAGAAC CACCCAAAGT  
26451 CACCTCTCCA ATGGTTACCT CTTTCAACAT A TGGACACC ATTGTTTCCA  
26501 CATCCATGCC TGGCTCCTCT GAGATTACAA GGATTGAGAT GGAGTCAACA  
26551 TTCTCCCTGG CTCATGGGCT GAAGGGAACC AGCACCTCCC AGGACCCCAT  
26601 CGTATCCACA GAGAAAAGTG CTGTCCTTCA CAAGTTGACC ACTGGTGCTA  
26651 CTGAGACCTC TAGGACAGAA GTTGCCTCTT CTAGAAGAAC ATCCATTCCA  
26701 GGCCCTGATC ATTCCACAGA GTCACCAGAC ATCTCCACTG AAGTGATCCC  
26751 CAGCCTGCCT ATCTCCCTTG GCATTACAGA ATCTTCAAAT ATGACCATCA  
26801 TCACTCGAAC AGGTCCTCCT CTTGGCTCTA CATCACAGGG CACATTTACC  
26851 TTGGACACAC CAACTACATC CTCCAGGGCA GGAACACACT CGATGGCGAC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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26901 TCAGGAATTT CCACACTCAG AAATGACCAC TGTCATGAAC AAGGACCCTG  
26951 AGATTCTATC ATGGACAATC CCTCCTTCTA TAGAGAAAAC CAGCTTCTCC  
27001 TCTTCCCTGA TGCCTTCACC AGCCATGACT TCACCTCCTG TTTCTCAAC  
27051 ATTACCAAAG ACCATTCA CA CACTCCTTC TCCTATGACC TCACTGCTCA  
27101 CCCCTAGCCT AGTGATGACC ACAGACACAT TGGGCACAAG CCCAGAACCT  
27151 ACAACCAGTT CACCTCCAAA TTTGAGCAGT ACCTCACATG AGATACTGAC  
27201 AACAGATGAA GACACCACAG CTATAGAAGC CATGCATCCT TCCACAAGCA  
27251 CAGCAGCGAC TAATGTGGAA ACCACCAGTT CTGGACATGG GTCACAATCC  
27301 TCTGTCCTAG CTGACTCAGA AAAAACCAAG GCCACAGCTC CAATGGATAC  
27351 CACCTCCACC ATGGGGCATA CAACTGTTTC CACATCAATG TCTGTTTCTT  
27401 CTGAGACTAC AAAAATTAAG AGAGAGTCAA CATATTCCTT GACTCCTGGA  
27451 CTGAGAGAGA CCAGCATTTC CCAAATGCC AGCTTTTCCA CTGACACAAG  
27501 TATTGTTCTT TCAGAAGTCC CCACTGGTAC TACTGCTGAG GTCTCCAGGA  
27551 CAGAAGTCAC CTCCTCTGGT AGAACATCCA TCCCTGGCCC TTCTCAGTCC  
27601 ACAGTTTTGC CAGAAATATC CACAAGAACA ATGACAAGGC TCTTTGCCTC  
27651 GCCCACCATG ACAGAATCAG CAGAAATGAC CATCCCCACT CAAACAGGTC  
27701 CTTCTGGGTC TACCTCACAG GATACCCTTA CCTTGGACAC ATCCACCACA  
27751 AAGTCCCAGG CAAAGACTCA TTCAACTTTG ACTCAGAGAT TTCCACACTC  
27801 AGAGATGACC ACTCTCATGA GCAGAGGTCC TGGAGATATG TCATGGCAAA  
27851 GCTCTCCCTC TCTGGAAAAT CCCAGCTCTC TCCCTTCCCT GCTGTCTTTA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
27901	<u>CCTGCCACAA CCTCACCTCC TCCCATTTC TCCACATTAC CAGTGACTAT</u>
27951	<u>CTCCTCCTCT CCTCTTCCTG TGA CTTCACCTCT AGCCCCGGTAA</u>
28001	<u>CGACCACAGA CATGTTACAC ACAAGCCCAG AACTTGTAAC CAGTTCACCT</u>
28051	<u>CCAAAGCTGA GCCACACTTC AGATGAGAGA CTGACCACTG GCAAGGACAC</u>
28101	<u>CACAAATACA GAAGCTGTGC ATCCTTCCAC AAACACAGCA GCGTCCAATG</u>
28151	<u>TGGAGATTCC CAGCTCTGGA CATGAATCCC CTCCTCTGC CTTAGCTGAC</u>
28201	<u>TCAGAGACAT CCAAAGCCAC ATCACCAATG TTTATTACCT CCACCCAGGA</u>
28251	<u>GGATACA ACT GTTGCCATAT CAACCCCTCA CTTCTTGGAG ACTAGCAGAA</u>
28301	<u> TTCAGAAAGA GTCAATTTCC TCCCTGAGCC CTAAATTGAG GGAGACAGGC</u>
28351	<u>AGTTCTGTGG AGACAAGCTC AGCCATAGAG ACAAGTGCTG TCCTTTCTGA</u>
28401	<u>AGTGTCCGTT GGTGCTACTA CTGAGATCTC CAGGACAGAA GTCACCTCCT</u>
28451	<u>CTAGCAGAAC ATCCATCTCT GGTTCGTCTG AGTCCACAAT GTTGCCAGAA</u>
28501	<u>ATATCCACCA CAAGAAAAAT CATTAAAGTTC CCTACTTCCC CCATCCTGGC</u>
28551	<u>AGAATCATCA GAAATGACCA TCAAGACCCA AACAAGTCCT CCTGGGTCTA</u>
28601	<u>CATCAGAGAG TACCTTTACA TTAGACACAT CAACCACTCC CTCCTTG GTA</u>
28651	<u>ATAACCCATT CGACTATGAC TCAGAGATTG CCACACTCAG AGATAACCAC</u>
28701	<u>TCTTGTGAGT AGAGGTGCTG GGGATGTGCC ACGGCCCAGC TCTCTCCCTG</u>
28751	<u>TGGAAGAAAC AAGCCCTCCA TCTTCCCAGC TGTCTTTATC TGCCATGATC</u>
28801	<u>TCACCTTCTC CTGTTTCTTC CACATTACCA GCAAGTAGCC ACTCCTCTTC</u>
28851	<u>TGCTTCTGTG ACTTCACTTC TCACACCAGG CCAAGTGAAG ACTACTGAGG</u>

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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28901 TGTTGGACGC AAGTGCAGAA CCTGAAACCA GTTCACCTCC AAGTTTGAGC  
28951 AGCACCTCAG TTGAAATACT GGCCACCTCT GAAGTCACCA CAGATACGGA  
29001 GAAAATTCAT CCTTTCTCAA ACACGGCAGT AACCAAAGTT GGAAGTTCCA  
29051 GTTCTGGACA TGAATCCCCT TCCTCTGTCC TACCTGACTC AGAGACAACC  
29101 AAAGCCACAT CGGCAATGGG TACCATCTCC ATTATGGGGG ATACAAGTGT  
29151 TTCTACATTA ACTCCTGCCT TATCTAACAC TAGGAAAATT CAGTCAGAGC  
29201 CAGCTTCCTC ACTGACCACC AGATTGAGGG AGACCAGCAC CTCTGAAGAG  
29251 ACCAGCTTAG CCACAGAAGC AAACACTGTT CTTTCTAAAG TGTCCACTGG  
29301 TGCTACTACT GAGGTCTCCA GGACAGAAGC CATCTCCTTT AGCAGAACAT  
29351 CCATGTCAGG CCCTGAGCAG TCCACAATGT CACAAGACAT CTCCATAGGA  
29401 ACCATCCCCA GGATTTCTGC CTCCTCTGTC CTGACAGAAT CTGCAAAAAT  
29451 GACCATCACA ACCCAAACAG GTCCTTCGGA GTCTACACTA GAAAGTACCC  
29501 TTAATTTGAA CACAGCAACC ACACCCTCTT GGGTGGAAC CCACTCTATA  
29551 GTAATTCAGG GATTTCCACA CCCAGAGATG ACCACTTCCA TGGGCAGAGG  
29601 TCCTGGAGGT GTGTCATGGC CTAGCCCTCC CTTTGTGAAA GAAACCAGCC  
29651 CTCCATCCTC CCCGCTGTCT TTACCTGCCG TGACCTCACC TCATCCTGTT  
29701 TCCACCACAT TCCTAGCACA TATCCCCCCC TCTCCCCCTC CTGTGACTTC  
29751 ACTTCTCACC TCTGGCCCCG CGACAACCAC AGATATCTTG GGTACAAGCA  
29801 CAGAACCTGG AACCAGTTCA TCTTCAAGTT TGAGCACCAC CTCCCATGAG  
29851 AGACTGACCA CTTACAAAGA CACTGCACAT ACAGAAGCCG TGCATCCTTC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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29901 CACAAACACA GGAGGGACCA ATGTGGCAAC CACCAGCTCT GGATATAAAT  
29951 CACAGTCCTC TGTCTAGCT GACTCATCTC CAATGTGTAC CACCTCCACC  
30001 ATGGGGGATA CAAGTGTCT CACATCAACT CTGCCTTCC TTGAGACTAG  
30051 GAGGATTCAG ACAGAGCTAG CTTCTCCCT GACCCCTGGA TTGAGGGAGT  
30101 CCAGTGGCTC TGAAGGGACC AGCTCAGGCA CCAAGATGAG CACTGTCCTC  
30151 TCTAAAGTGC CCACTGGTGC TACTACTGAG ATCTCCAAGG AAGACGTCAC  
30201 CTCCATCCCA GGTCCCCTC AATCCACAAT ATCACCAGAC ATCTCCACAA  
30251 GAACCGTCAG CTGGTCTCT ACATCCCCTG TCATGACAGA ATCAGCAGAA  
30301 ATAACCATGA ACACCCATAC AAGTCCTTTA GGGGCCACAA CACAAGGCAC  
30351 CAGTACTTTG GCCACGTCAA GCACAACCTC TTTGACAATG ACACACTCAA  
30401 CTATATCTCA AGGATTTTCA CACTCACAGA TGAGCACTCT TATGAGGAGG  
30451 GGTCCTGAGG ATGTATCATG GATGAGCCCT CCCCTTCTGG AAAAACTAG  
30501 ACCTTCCTTT TCTCTGATGT CTTACCAGC CACAATTCA CCTTCTCCTG  
30551 TTTCTCCAC ATTACCAGAG AGCATCTCTT CCTCTCCTCT TCCTGTGACT  
30601 TCACTCCTCA CGTCTGGCTT GGCAAAAACCT ACAGATATGT TGCACAAAAG  
30651 CTCAGAACCT GTAACCAACT CACCTGCAAA TTTGAGCAGC ACCTCAGTTG  
30701 AAATACTGGC CACCTCTGAA GTCACCACAG ATACAGAGAA AACTCATCCT  
30751 TCTTCAAACA GAACAGTGAC CGATGTGGGG ACCTCCAGTT CTGGACATGA  
30801 ATCCACTTCC TTTGTCCTAG CTGACTCACA GACATCCAAA GTCACATCTC  
30851 CAATGGTTAT TACCTCCACC ATGGAGGATA CGAGTGTCTC CACATCAACT

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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30901 CCTGGCTTTT TTGAGACTAG CAGAATTCAG ACAGAACCAA CATCCTCCCT  
30951 GACCTTGGA CTGAGAAAGA CCAGCAGCTC TGAGGGGACC AGCTTAGCCA  
31001 CAGAGATGAG CACTGTCCTT TCTGGAGTGC CCACTGGTGC CACTGCTGAA  
31051 GTCTCCAGGA CAGAAGTCAC CTCCTCTAGC AGAACATCCA TCTCAGGCTT  
31101 TGCTCAGCTC ACAGTGTAC CAGAGACTTC CACAGAAACC ATCACCAGAC  
31151 TCCCTACCTC CAGCATAATG ACAGAATCAG CAGAAATGAT GATCAAGACA  
31201 CAAACAGATC CTCCTGGGTC TACACCAGAG AGTACTCATA CTGTGGACAT  
31251 ATCAACAACA CCCAACTGGG TAGAAACCCA CTCGACTGTG ACTCAGAGAT  
31301 TTTCACACTC AGAGATGACC ACTCTTGTA GCAGAAGCCC TGGTGATATG  
31351 TTATGGCCTA GTCAATCCTC TGTGGAAGAA ACCAGCTCTG CCTCTTCCCT  
31401 GCTGTCTCTG CCTGCCACGA CCTCACCTTC TCCTGTTTCC TCTACATTAG  
31451 TAGAGGATTT CCCTTCCGCT TCTCTTCTG TGACTTCTCT TCTCACCCTT  
31501 GGCCTGGTGA TAACCACAGA CAGGATGGGC ATAAGCAGAG AACCTGGAAC  
31551 CAGTTCCACT TCAAATTTGA GCAGCACCTC CCATGAGAGA CTGACCACTT  
31601 TGGAAGACAC TGTAATATACA GAAGACATGC AGCCTTCCAC ACACACAGCA  
31651 GTGACCAACG TGAGGACCTC CATTTCTGGA CATGAATCAC AATCTTCTGT  
31701 CCTATCTGAC TCAGAGACAC CCAAAGCCAC ATCTCCAATG GGTACCACCT  
31751 ACACCATGGG GGAAACGAGT GTTCCATAT CCACTTCTGA CTTCCTTGAG  
31801 ACCAGCAGAA TTCAGATAGA ACCAACATCC TCCCTGACTT CTGGATTGAG  
31851 GGAGACCAGC AGCTCTGAGA GGATCAGCTC AGCCACAGAG GGAAGCACTG

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
<hr/>	
31901	<u>TCCTTTCTGA AGTGCCAGT GGTGCTACCA CTGAGGTCTC CAGGACAGAA</u>
31951	<u>GTGATATCCT CTAGGGGAAC ATCCATGTCA GGGCCTGATC AGTTCACCAT</u>
32001	<u>ATCACCAGAC ATCTCTACTG AAGCGATCAC CAGGCTTTCT ACTTCCCCCA</u>
32051	<u>TTATGACAGA ATCAGCAGAA AGTGCCATCA CTATTGAGAC AGGTTCTCCT</u>
32101	<u>GGGGCTACAT CAGAGGGTAC CCTCACCTTG GACACCTCAA CAACAACCTT</u>
32151	<u>TTGGTCAGGG ACCCACTCAA CTGCATCTCC AGGATTTTCA CACTCAGAGA</u>
32201	<u>TGACCACTCT TATGAGTAGA ACTCCTGGAG ATGTGCCATG GCCGAGCCTT</u>
32251	<u>CCCTCTGTGG AAGAAGCCAG CTCTGTCTCT TCCTCACTGT CTTCACTGC</u>
32301	<u>CATGACCTCA ACTTCTTTTT TCTCCACATT ACCAGAGAGC ATCTCCTCCT</u>
32351	<u>CTCCTCATCC TGTGACTGCA CTTCTACCC TTGGCCCAGT GAAGACCACA</u>
32401	<u>GACATGTTGC GCACAAGCTC AGAACCTGAA ACCAGTTCAC CTCCAAATTT</u>
32451	<u>GAGCAGCACC TCAGCTGAAA TATTAGCCAC GTCTGAAGTC ACCAAAGATA</u>
32501	<u>GAGAGAAAAT TCATCCCTCC TCAAACACAC CTGTAGTCAA TGTAGGGACT</u>
32551	<u>GTGATTTATA AACATCTATC CCCTTCCTCT GTTTTGGCTG ACTTAGTGAC</u>
32601	<u>AACAAAACCC ACATCTCCAA TGGCTACCAC CTCCACTCTG GGGAATACAA</u>
32651	<u>GTGTTTCCAC ATCAACTCCT GCCTTCCCAG AAACATATGAT GACACAGCCA</u>
32701	<u>ACTTCCTCCC TGAATTCTGG ATTAAGGGAG ATCAGTACCT CTCAAGAGAC</u>
32751	<u>CAGCTCAGCA ACAGAGAGAA GTGCTTCTCT TTCTGGAATG CCCACTGGTG</u>
32801	<u>CTACTACTAA GGTCTCCAGA ACAGAAGCCC TCTCCTTAGG CAGAACATCC</u>
32851	<u>ACCCAGGTC CTGCTCAATC CACAATATCA CCAGAAATCT CCACGGAAAC</u>

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Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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32901 CATCACTAGA ATTTCTACTC CCCTCACCAC GACAGGATCA GCAGAAATGA

32951 CCATCACCCC CAAAACAGGT CATTCTGGGG CATCCTCACA AGGTACCTTT

33001 ACCTTGGA CA CATCAAGCAG AGCCTCCTGG CCAGGAACTC ACTCAGCTGC

33051 AACTCACAGA TCTCCACACT CAGGGATGAC CACTCCTATG AGCAGAGGTC

33101 CTGAGGATGT GTCATGGCCA AGCCGCCCAT CAGTGGA AAA AACTAGCCCT

33151 CCATCTTCCC TGGTGTCTTT ATCTGCAGTA ACCTCACCTT CGCCACTTTA

33201 TTCCACACCA TCTGAGAGTA GCCACTCATC TCCTCTCCGG GTGACTTCTC

33251 TTTTCACCCC TGTCATGATG AAGACCACAG ACATGTTGGA CACAAGCTTG

33301 GAACCTGTGA CCACTTCACC TCCAGTATG AATATCACCT CAGATGAGAG

33351 TCTGGCCACT TCTAAAGCCA CCATGGAGAC AGAGGCAATT CAGCTTTCAG

[0056] 33401 AAAACACAGC TGTGACTCAG ATGGGCACCA TCAGCGCTAG  
ACAAGAATTC

33451 TATTCCTCTT ATCCAGGCCT CCCAGAGCCA TCCAAAGTGA CATCTCCAGT

33501 GGTCACCTCT TCCACCATAA AAGACATTGT TTCTACAACC ATACCTGCTT

33551 CCTCTGAGAT AACAAGAATT GAGATGGAGT CAACATCCAC CCTGACCCCC

33601 ACACCAAGGG AGACCAGCAC CTCCCAGGAG ATCCACTCAG CCACAAAGCC

33651 AAGCACTGTT CTTACAAGG CACTCACTAG TGCCACGATT GAGGACTCCA

33701 TGACACAAGT CATGTCCTCT AGCAGAGGAC CTAGCCCTGA TCAGTCCACA

33751 ATGTCACAAG ACATATCCAG TGAAGTGATC ACCAGGCTCT CTACCTCCCC

33801 CATCAAGGCA GAATCTACAG AAATGACCAT TACCACCCAA ACAGGTTCTC

33851 CTGGGGCTAC ATCAAGGGGT ACCCTTACCT TGGACACTTC AACAACTTTT



Table 1 (continued)

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**Genomic CA125 Amino Terminal Sequence**  
(SEQ ID NO: 1)

---

33901 ATGTCAGGGA CCCACTCAAC TGCATCTCAA GGATTTTCAC ACTCACAGAT

33951 GACCGCTCTT ATGAGTAGAA CTCCTGGAGA TGTGCCATGG CTAAGCCATC

34001 CCTCTGTGGA AGAAGCCAGC TCTGCCTCTT TCTCACTGTC TTCACCTGTC

34051 ATGACCTCAT CTTCTCCCGT TTCTTCCACA TTACCAGACA GCATCCACTC

34101 TTCTTCGCTT CCTGTGACAT CACTTCTCAC CTCAGGGCTG GTGAAGACCA

34151 CAGAGCTGTT GGGCACAAGC TCAGAACCTG AAACCAGTTC ACCCCCAAAT

34201 TTGAGCAGCA CCTCAGCTGA AATACTGGCC ACCACTGAAG TCACTACAGA

34251 TACAGAGAAA CTGGAGATGA CCAATGTGGT AACCTCAGGT TATACACATG

34301 AATCTCCTTC CTCTGTCCTA GCTGACTCAG TGACAACAAA GGCCACATCT

34351 TCAATGGGTA TCACCTACCC CACAGGAGAT ACAAATGTTC TCACATCAAC

34401 CCCTGCCTTC TCTGACACCN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

34451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NI NNNNNNNNN NNNNNNNNNN

34501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNCGGAAA CCAAGTTTCT

**Exon 4**

34551 AACCAACCCC TCCTTTTTGA CCCAGTAGG ATTCAAACAA AGTCAAAGCT

34601 CTCACTGACT CCTGGGTTGA TGGAGACCAG CATCTCTGAA GAGACCAGCT

34651 CTGCCACAGA AAAAAGCACT GTCCTTTCTA GTGTGCCCAC TGGTGCTACT

34701 ACTGAGGTCT CCAGGACAGA AGCCATCTCT TCTAGCAGAA CATCCATCCC

34751 AGGCCCTGCT CAATCCACAA TGTCATCAGA CACCTCCATG GAAACCATCA

34801 CTAGAAATTC TACCCCCCTC ACAAGGAAAG AATCAACAGA CATGGCCATC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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34851 ACCCCCAAA CAGGTCCTTC TGGGGCTACC TCGCAGGGTA CCTTTACCTT  
34901 GGACTCATCA AGCACAGCCT CCTGGCCAGG AACTCACTCA GCTACAATC  
34951 AGAGATTTCC ACAGTCAGTG GTGACAACTC CTATGAGCAG AGGTCCTGAG  
35001 GATGTGTCAT GGCCAAGCCC GCTGTCTGTG GAAAAAACA GCCCTCCATC  
35051 TTCCCTGGTA TCTTCATCTT CAGTAACCTC ACCTTCGCCA CTTTATTCCA  
35101 CACCATCTGG GAGTAGCCAC TCCTCTCCTG TCCCTGTCAC TTCTCTTTTC  
35151 ACCTCTATCA TGATGAAGGC CACAGACATG TTGGATGCAA GTTTGGAACC  
35201 TGAGACCACT TCAGCTCCCA ATATGAATAT CACCTCAGAT GAGAGTCTGG  
35251 CCACTTCTAA AGCCACCACG GAGACAGAGG CAATTCACGT TTTTGAAAAT  
35301 ACAGCAGCGT CCCATGTGGA AACCACCAGT GCTACAGAGG AACTCTATTC  
35351 CTCTTCCCCA GGCTTCTCAG AGCCAACAAA AGTGATATCT CCAGTGGTCA  
35401 CCTCTTCCTC TATAAGAGAC AACATGGTTT CCACAACAAT GCCTGGCTCC  
35451 TCTGGCATT AAGGATTGA GATAGAGTCA ATGTCATCTC TGACCCCTGG  
35501 ACTGAGGGAG ACCAGAACCT CCCAGGACAT CACCTCATCC ACAGAGACAA  
35551 GCACTGTCCT TTACAAGATG TCCTCTGGTG CCACTCCTGA GGTCTCCAGG  
35601 ACAGAAGTTA TGCCCTCTAG CAGAACATCC ATTCCTGGCC CTGCTCAGTC  
35651 CACAATGTCA CTAGACATCT CCGATGAAGT TGTACCAGG CTGTCTACCT  
35701 CTCCCATCAT GACAGAATCT GCAGAAATAA CCATCACCAC CCAAACAGGT  
35751 TATTCTCTGG CTACATCCCA GGTTACCCCT CCCTTGGGCA CCTCAATGAC  
35801 CTTTTTGTCA GGGACCCACT CAACTATGTC TCAAGGACTT TCACACTCAG

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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35851 AGATGACCAA TCTTATGAGC AGGGGTCCTG AAAGTCTGTC ATGGACGAGC  
35901 CCTCGCTTTG TGGAAACAAC TAGATCTTCC TCTTCTCTGA CATCATTACC  
35951 TCTCACGACC TCACTTTCTC CTGTGTCCTC CACATTACTA GACAGTAGCC  
36001 CCTCCTCTCC TCTTCCTGTG ACTTCACTTA TCCTCCCAGG CCTGGTGAAG  
36051 ACTACAGAAG TGTTGGATAC AAGCTCAGAG CCTAAAACCA GTTCATCTCC  
36101 AAATTTGAGC AGCACCTCAG TTGAAATACC GGCCACCTCT GAAATCATGA  
36151 CAGATACAGA GAAAATTCAT CCTTCCTCAA ACACAGCGGT GGCCAAAGTG  
36201 AGGACCTCCA GTTCTGTTCA TGAATCTCAT TCCTCTGTCC TAGCTGACTC  
36251 AGAAACAACC ATAACCATAC CTTCAATGGG TATCACCTCC GCTGTGGACG  
36301 ATACCACTGT TTTCACATCA AATCCTGCCT TCTCTGAGAC TAGGAGGATT  
36351 CCGACAGAGC CAACATTCTC ATTGACTCCT GGATTGAGG AGACTAGCAC  
36401 CTCTGAAGAG ACCACCTCAA TCACAGAAAC AAGTGCAGTC CTTTATGGAG  
36451 TGCCCACTAG TGCTACTACT GAAGTCTCCA TGACAGAAAT CATGTCCTCT  
36501 AATAGAACAC ACATCCCTGA CTCTGATCAG TCCACGATGT CTCCAGACAT  
36551 CATCACTGAA GTGATCACCA GGCTCTCTTC CTCATCCATG ATGTCAGAAT  
36601 CAACACAAAT GACCATCACC ACCCAAAAAA GTTCTCCTGG GGCTACAGCA  
36651 CAGAGTACTC TTACCTTGGC CACAACAACA GCCCCCTTGG CAAGGACCCA  
36701 CTCAACTGTT CCTCCTAGAT TTTTACACTC AGAGATGACA ACTCTTATGA  
36751 GTAGGAGTCC TGAAAATCCA TCATGGAAGA GCTCTCCCTT TGTGGAAAAA  
36801 ACTAGCTCTT CATCTTCTCT GTTGTCTTA CCTGTCACGA CCTCACCTTC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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36851 TGTTTCTTCC ACATTACCGC AGAGTATCCC TTCCTCCTCT TTTTCTGTGA  
36901 CTTCACTCCT CACCCAGGC ATGGTGAAGA CTACAGACAC AAGCACAGAA  
36951 CCTGGAACCA GTTTATCTCC AAATCTGAGT GGCACCTCAG TTGAAATACT  
37001 GGCTGCCTCT GAAGTCACCA CAGATACAGA GAAAATTCAT CCTTCTTCAA  
37051 GCATGGCAGT GACCAATGTG GGAACCACCA GTTCTGGACA TGAATATAT  
37101 TCCTCTGTTT CAATCCACTC GGAGCCATCC AAGGCTACAT ACCCAGTGGG  
37151 TACTCCCTCT TCCATGGCTG AAACCTCTAT TTCCACATCA ATGCCTGCTA  
37201 ATTTTGAGAC CACAGGATTT GAGGCTGAGC CATTTTCTCA TTTGACTTCT  
37251 GGATTTAGGA AGACAAACAT GTCCCTGGAC ACCAGCTCAG TCACACCAAC  
37301 AAATACACCT TCTTCTCCTG GGTCCACTCA CCTTTTACAG AGTTCCAAGA  
37351 CTGATTTTAC CTCTTCTGCA AAAACATCAT CCCCAGACTG GCCTCCAGCC  
37401 TCACAGTATA CTGAAATTCC AGTGGACATA ATCACCCCTT TTAATGCTTC  
37451 TCCATCTATT ACGGAGTCCA CTGGGATAAC CTCCTTCCCA GAATCCAGGT  
37501 TTACTATGTC TGTAACAGAA AGTACTCATC ATCTGAGTAC AGATTGCTG  
37551 CCTTCAGCTG AGACTATTTT CACTGGCACA GTGATGCCTT CTCTATCAGA  
37601 GGCCATGACT TCATTTGCCA CCACTGGAGT TCCACGAGCC ATCTCAGGTT  
37651 CAGGTAGTCC ATTCTCTAGG ACAGAGTCAG GCCCTGGGGA TGCTACTCTG  
37701 TCCACCATTG CAGAGAGCCT GCCTTCATCC ACTCCTGTGC CATTCTCCTC  
37751 TTCAACCTTC ACTACCACTG ATTCTTCAAC CATCCCAGCC CTCCATGAGA  
37801 TAACTTCCTC TTCAGCTACC CCATATAGAG TGGACACCAG TCTTGGGACA

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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37851 GAGAGCAGCA CTACTGAAGG ACGCTTGGTT ATGGTCAGTA CTTTGGACAC  
 37901 TTCAAGCCAA CCAGGCAGGA CATCTTCAAC ACCCATTTTG GATACCAGAA  
 37951 TGACAGAGAG CGTTGAGCTG GGAACAGTGA CAAGTGCTTA TCAAGTTCCT  
 38001 TCACTCTCAA CACGGTTGAC AAGAGAATGC GCATGGCGAG AAGGGAGAAG  
 38051 TGTAGTTGGA TGGATAAAAG GAAGAATGGA GAGAAGAGTG AATGGAAGGA  
 38101 AGCAAAGATG AAGCGGAGGA AGGATAGATG CACAGAAGGA AGGATGAAAA  
 38151 GAAAGAAAGA TGATGGAAGA CAGGATTGAA GGGGATATAG ATTGAAGGAA  
 38201 AGAAAGGTAG AAGGATGAAA TGAAGTAAAG ATTGAAGAAA AGATGGATGG  
 38251 AAAGAAGAAA GGAGGGTGCA CAAAAAATCT CACACTTCAC CACATATGAT  
 38301 TCATCCATAT AAGAAAAAAC CACTTGTACC CTCAAAGCTA TTGAAATACA  
 38351 AACTTTTAAA TTAAAATTTT AAAAAGCAAG AGAAAGGAAA GAAGGGAGGA  
 38401 AAGACAAAAG GAAGAATGGG TGATAGAAGG AAAGAATAAA AGGAAGAAAA  
 38451 AATGGAAGAA TAGATGATCA GATCTAGGGA TGAATGAAAG GAAGGATGGA  
 38501 CAAATCTATA GGTAGGTGGA TGGATCTATG GACAGGTGTG GCCACTTATG  
 38551 GCACATAGTC CCAGCTCCAG TTCATACTGA TGGACTTGAG GAGTGTTTGT  
 38601 GGCCAATGAA GTGGATCCAT TTAGACAGTG CTCTTCTTCT GAATGAGATG

**Exon 5**

38651 AGTTACCCCA GTTTTTCTCC CCACCTTCAT CTTCAGGAAC TGATGGCATT  
 38701 ATGGAACACA TCACAAAAAT ACCCAATGAA GCAGCACACA GAGGTACCAT  
 38751 AAGACCAGTC AAAGGCCCTC AGACATCCAC TTCGCCTGCC AGTCCTAAAG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
38801	GTAGGTTTAA	CTTTGCTTAC	CTCCCAGTAA	TGCCACTCGT	GACCATATTT
38851	CCTCCTCCAG	AGAGACAAAA	TGTTTGTATT	CTTTAGAGAG	AGAATTGTGT
38901	GTGGTTGTCA	TAGGTTTCCC	TGTCTGAACT	GAGTCTTTAT	CTAATGGTTA
38951	CCAGGCAGAT	GTTACCACTG	TCTCTTTCTC	CTCATGGCAT	GCTGAGTGAG
39001	TTTTGTCCAA	CATCAAATAT	TCACAAATTT	GTCCATATTA	ACCAAATTTT
39051	AAAAATGCTC	ATTAAAAACT	TACTATGAGC	TGGGCGCAGT	GGCTCATGCC
39101	TGTAATCCCA	ATACTTTGGG	AGGCTGAGCT	GGGTGGATCA	CCAGAGGTCA
39151	AAAATTGAG	ACCAGTCTGA	CCAAAATGGT	GAAACTCCAT	CTCTACTGAA
39201	AATATAAAAA	TTAGCCGGGC	ATGGTGGCAC	ACACCGTAAT	CACAGCTACT
39251	CAGGAGGCTG	AGGCAAGAGA	GTCACCTGAA	CCACAGGAGG	TAGAGGCTGC
39301	AGTGAGCTGA	GCATTGTGCC	AATGCACTCC	AGCCTGGGTG	GCAGAGCAAG
39351	ACTCCAGCTC	AGAAATAAAT	AATATATTAT	ATATATATAT	ATATGTTTTA
39401	TTTAGATGGA	ATATACTATA	TATATATGTA	TATATATATG	TATGTATATA
39451	TATATATGTA	TGTATATATA	TATATATATA	TATATATATA	TATATAGAGA
39501	GAGAGAGAGA	GAGAGAGAGA	GAGAGAGACA	GAGTATGTCT	GAGAATGCAT
39551	CCCGATAGTT	CTAGCAAGGT	AGGAAAAGGA	AGTATCATAA	CAGCCTTGAA
39601	GTAGCCTGTT	GAAACAGACA	GACTCTCTTG	TAAGAGAACT	CACAAAATCT
39651	AGGATTATAT	CTCCCATGAT	GAAAAATTTG	GAACTGTACA	TTTTTGTTTA
39701	ACTGTCACTT	AAATNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
39751	NNNNNNNNNN	NNNNNNNNNN	NCCAGGAGGC	ACTGTGCTTG	GCGCCTTTTT

Table 1 (continued)

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**Genomic CA125 Amino Terminal Sequence**  
(SEQ ID NO: 1)

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39801 ACCAACACTT TGAGATGGCC ATTGTACTTA TCCCCACTTT ATAGACGGGA  
 39851 AAATGGAGGT CCAGCAATAT TTTTAACTT AAAGAGCCAC CCATCTCTTT  
 39901 AGAGAAAGAG CCAGAATCCC AGGCAGGGGC TATCTTATTC CAGAGCCCAA  
 39951 GCTCTCAAAC ACATGATACA CAATACTTAA TCTCTCTCAA GTCAGAGGAG  
 40001 ATCCACTTAA GTATACATCC ATCCACATAT TCATTCATTC AATCATTCAA  
 40051 CAAATATTAG TTGAGCACTT ACCGTATGCC AAACAGTCAA ACGTGAATAG  
 40101 CTGTTACAAA TGAGACTGTG AAGGATGGTA CAACGCAGAT TCAGACAGTG  
 40151 TGATAAGGAA ATATTGAGAA GCAAAGATGA GTTCTGGAGT GAATTTGTAA  
 40201 AGGTGGATGT GGGCTTGGAT TTCAATAATG GCAGAACTTA AGGAATCTGA  
 40251 TGAGAAGTGG GCACTTCAGG CAGAGAGAAG AGCTTGAACA AGGCTCAGAG  
 40301 GCTGACAGTG CAGGAAACAC ATGGGAAGAG GGAATAGAGT AGCGGTCAAG  
 40351 AATTCACAGA GGAGTTATAG GTGAAGATGC AACCAAGTTA CAGACCAAGG  
 40401 TAAGATAGGG GAATACCAAT CACAATCTCT TTTCCCATTC CAGAAGCATC  
 40451 CCAGACACAT CCTAGTAACC GAGAGACATT TCTCTCCCTT TCCTCCTGTG  
 40501 GAGAATAAAT AAGCTATTGC AAGTCCAGTA AGTGTAATCA TTTTGTTCAA

**Exon 6**

40551 ATTGTGTGCC CATTCCCCAA TTTACAGGAC TACACACAGG AGGGACAAAA  
 40601 AGAATGGAGA CCACAACCAC AGCTCTGAAG ACCACCACCA CAGCTCTGAA  
 40651 GACCACTTCC AGAGCCACCT TGACCACCAG TGTCTATACT CCCACTTTGG  
 40701 GAACACTGAC TCCCCTCAAT GCATCAATGC AAATGGCCAG CACAATCCCC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
40751	<u>ACAGAAATGA TGATCACAAC CCCATATGTT TTCCCTGATG TTCCAGAAAC</u>
40801	<u>GACATCCTCA TTGGCTACCA GCCTGGGAGC AGAAACCAGC ACAGCTCTTC</u>
40851	<u>CCAGGACAAC CCCATCTGTT TTCAATAGAG AATCAGAGAC CACAGCCTCA</u>
40901	<u>CTGGTCTCTC GTTCTGGGGC AGAGAGAAGT CCGGTTATTC AAACCTCTAGA</u>
40951	<u>TGTTTCTTCT AGTGAGCCAG ATACAACAGC TTCATGGGTT ATCCATCCTG</u>
41001	<u>CAGAGACCAT CCCAACTGTT TCCAAGACAA CCCCCAATTT TTTCCACAGT</u>
41051	<u>GAATTAGACA CTGTATCTTC CACAGCCACC AGTCATGGGG CAGACGTCAG</u>
41101	<u>CTCAGCCATT CCAACAAATA TCTCACCTAG TGAAC TAGAT GCACTGACCC</u>
41151	<u>CACTGGTCAC TATTTCTGGGG ACAGATACTA GTACAACATT CCCAACACTG</u>
41201	<u>ACTAAGTCCC CACATGAAAC AGAGACAAGA ACCACATGGC TCACTCATCC</u>
41251	<u>TGCAGAGACC AGCTCAACTA TTCCAGAAC AATCCCCAAT TTTTCTCATC</u>
41301	<u>ATGAATCAGA TGCCACACCT TCAATAGCCA CCAGTCCTGG GGCAGAAACC</u>
41351	<u>AGTTCAGCTA TTCCAATTAT GACTGTCTCA CCTGGTGCAG AAGATCTGGT</u>
41401	<u>GACCTCACAG GTCACTAGTT CTGGGACAGA CAGAAATATG ACTATTCCAA</u>
41451	<u>CTTTGACTCT TTCTCCTGGT GAACCAAAGA CGATAGCCTC ATTAGTCACC</u>
41501	<u>CATCCTGAAG CACAGACAAG TTCGGCCATT CCAACTTCAA CTATCTCGCC</u>
41551	<u>TGCTGTATCA CGGTGGTGA CCTCAATGGT CACCAGTTTG GCGGCAAAGA</u>
41601	<u>CAAGTACAAC TAATCGAGCT CTGACAACT CCCCTGGTGA ACCAGCTACA</u>
41651	<u>ACAGTTTCAT TGGTCACGCA TCCTGCACAG ACCAGCCCAA CAGTTCCCTG</u>
41701	<u>GACAACTTCC ATTTTTTTTCC ATAGTAAATC AGACACCACA CCTTCAATGA</u>



Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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41751 CCACCAGTCA TGGGGCAGAA TCCAGTTCAG CTGTTCCAAC TCCAAGTGT  
41801 TCAACTGAGG TACCAGGAGT AGTGACCCCT TTGGTCACCA GTTCTAGGGC  
41851 AGTGATCAGT ACAACTATTC CAATTCTGAC TCTTTCTCCT GGTGAACCAG  
41901 AGACCACACC TTCAATGGCC ACCAGTCATG GGGAAGAAGC CAGTTCTGCT  
41951 ATTCCAAGTC CAACTGTTTC ACCTGGGGTA CCAGGAGTGG TGACCTCTCT  
42001 GGTCACTAGT TCTAGGGCAG TGACTAGTAC AACTATTCCA ATTCTGACTT  
42051 TTTCTCTTGG TGAACCAGAG ACCACACCTT CAATGGCCAC CAGTCATGGG  
42101 ACAGAAGCTG GCTCAGCTGT TCCAAGTGT TTACCTGAGG TACCAGGAAT  
42151 GGTGACCTCT CTGGTTGCTA GTTCTAGGGC AGTAACCACT ACAACTCTTC  
42201 CAACTCTGAC TCTTTCTCCT GGTGAACCAG AGACCACACC TTCAATGGCC  
42251 ACCAGTCATG GGGCAGAAGC CAGCTCAACT GTTCCAAGT TTTACCTGA  
42301 GGTACCAGGA GTGGTGACCT CTCTGGTCAC TA TTCTAGT GGAGTAAACA  
42351 GTACAAGTAT TCCAAGTCTG ATTCTTTCTC CTGGTGAACT AGAAACCACA  
42401 CCTTCAATGG CCACCAGTCA TGGGGCAGAA GCCAGCTCAG CTGTTCCAAC  
42451 TCCAAGTGT TCACCTGGGG TATCAGGAGT GGTGACCCCT CTGGTCACTA  
42501 GTTCCAGGGC AGTGACCAGT ACAACTATTC CAATTCTAAC TCTTTCTTCT  
42551 AGTGAGCCAG AGACCACACC TTCAATGGCC ACCAGTCATG GGGTAGAAGC  
42601 CAGCTCAGCT GTTCTAACTG TTTACCTGA GGTACCAGGA ATGGTGACCT  
42651 CTCTGGTCAC TAGTTCTAGA GCAGTAACCA GTACAACTAT TCCAAGTCTG  
42701 ACTATTTCTT CTGATGAACC AGAGACCACA ACTTCATTGG TCACCCATTC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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42751 TGAGGCAAAG ATGATTTTCAG CCATTCCAAC TTTAGCTGTC TCCCCTACTG  
42801 TACAAGGGCT GGTGACTTCA CTGGTCACTA GTTCTGGGTC AGAGACCAGT  
42851 GCGTTTTTCAA ATCTAACTGT TGCCTCAAGT CAACCAGAGA CCATAGACTC  
42901 ATGGGTCGCT CATCCTGGGA CAGAAGCAAG TTCTGTTGTT CCAACTTTGA  
42951 CTGTCTCCAC TGGTGAGCCG TTTACAAATA TCTCATTGGT CACCCATCCT  
43001 GCAGAGAGTA GCTCAACTCT TCCCAGGACA ACCTCAAGGT TTTCCACAG  
43051 TGAATTAGAC ACTATGCCTT CTACAGTCAC CAGTCCTGAG GCAGAATCCA  
43101 GCTCAGCCAT TTCAACAACT ATTTACCTG GTATACCAGG TGTGCTGACA  
43151 TCACTGGTCA CTAGCTCTGG GAGAGACATC AGTGCAACTT TTCCAACAGT  
43201 GCCTGAGTCC CCACATGAAT CAGAGGCAAC AGCCTCATGG GTTACTCATC  
43251 CTGCAGTCAC CAGCACAACA GTTCCCAGGA CAACCCCTAA TTATTCTCAT  
43301 AGTGAACCAG ACACCACACC ATCAATAGCC ACCAGTCCTG GGGCAGAAGC  
43351 CACTTCAGAT TTTCCAACAA TAACTGTCTC ACCTGATGTA CCAGATATGG  
43401 TAACCTCACA GGTCAGTAGT TCTGGGACAG ACACCAGTAT AACTATTCCA  
43451 ACTCTGACTC TTTCTTCTGG TGAGCCAGAG ACCACAACCT CATTTATCAC  
43501 CTATTCTGAG ACACACACAA GTTCAGCCAT TCCAACCTC CCTGTCTCCC  
43551 CTGGTGCATC AAAGATGCTG ACCTCACTGG TCATCAGTTC TGGGACAGAC  
43601 AGCACTACAA CTTTCCCAAC ACTGACGGAG ACCCCATATG AACCAGAGAC  
43651 AACAGCCATA CAGCTCATTC ATCCTGCAGA GACCAACACA ATGGTTCCCA  
43701 GGACAACTCC CAAGTTTTC CATAGTAAGT CAGACACCAC ACTCCCAGTA

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
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43751	<u>GCCATCACCA GTCCTGGGCC AGAAGCCAGT TCAGCTGTTT CAACGACAAC</u>
43801	<u>TATCTCACCT GATATGTCAG ATCTGGTGAC CTCACTGGTC CCTAGTTCCTG</u>
43851	<u>GGACAGACAC CAGTACAACC TTCCCAACAT TGAGTGAGAC CCCATATGAA</u>
43901	<u>CCAGAGACTA CAGCCACGTG GCTCACTCAT CCTGCAGAAA CCAGCACAAC</u>
43951	<u>GGTTTCTGGG ACAATTCCCA ACTTTTCCCA TAGGGGATCA GACACTGCAC</u>
44001	<u>CCTCAATGGT CACCAGTCCT GGAGTAGACA CGAGGTCAGG TGTTCCTCACT</u>
44051	<u>ACAACCATCC CACCCAGTAT ACCAGGGGTA GTGACCTCAC AGGTCCTAG</u>
44101	<u>TTCTGCAACA GACACTAGTA CAGCTATTCC AACTTTGACT CCTTCTCCTG</u>
44151	<u>GTGAACCAGA GACCACAGCC TCATCAGCTA CCCATCCTGG GACACAGACT</u>
44201	<u>GGCTTCACTG TTCCAATTCG GACTGTTCCC TCTAGTGAGC CAGATACAAT</u>
44251	<u>GGCTTCCTGG GTCATCATC CTCCACAGAC CAGCACACCT GTTTCAGAA</u>
44301	<u>CAACCTCCAG TTTTTCCTAT AGTAGTCCAG ATGCCACACC TGTAATGGCC</u>
44351	<u>ACCAGTCCTA GGACAGAAGC CAGTTCAGCT GTACTGACAA CAATCTCACC</u>
44401	<u>TGGTGACCA GAGATGGTGA CTTACAGAT CACTAGTTCT GGGGCAGCAA</u>
44451	<u>CCAGTACAAC TGTTCCTCACT TTGACTCATT CTCCTGGTAT GCCAGAGACC</u>
44501	<u>ACAGCCTTAT TGAGCACCCA TCCAGAACA GAGACAAGTA AAACATTTCC</u>
44551	<u>TGCTTCAACT GTGTTTCCTC AAGTATCAGA GACCACAGCC TCACTCACCA</u>
44601	<u>TTAGACCTGG TGCAGAGACT AGCACAGCTC TCCCAACTCA GACAACATCC</u>
44651	<u>TCTCTCTTCA CCCTACTTGT AACTGGAACC AGCAGAGTTG ATCTAAGTCC</u>
44701	<u>AACTGCTTCA CCTGGTGTTT CTGCAAAAAC AGCCCCACTT TCCACCCATC</u>

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Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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44751 CAGGGACAGA AACCAGCACA ATGATTCCAA CTTCAACTCT TTCCCTTGGT  
44801 TTACTAGAGA CTACAGGCTT ACTGGCCACC AGCTCTTCAG CAGAGACCAG  
44851 CACGAGTACT CTAACCTCTGA CTGTTTCCCC TGCTGTCTCT GGGCTTTCCA  
44901 GTGCCTCTAT AACAACTGAT AAGCCCCAAA CTGTGACCTC CTGGAACACA  
44951 GAAACCTCAC CATCTGTAAC TTCAGTTGGA CCCCAGAAT TTTCCAGGAC  
45001 TGTCACAGGC ACCACTATGA CCTTGATACC ATCAGAGATG CCAACACCAC  
45051 CTAAAACCAG TCATGGAGAA GGAGTGAGTC CAACCACTAT CTTGAGAACT  
45101 ACAATGGTTG AAGCCACTAA TTTAGCTACC ACAGGTTCCA GTCCCACTGT  
45151 GGCCAAGACA ACAACCACCT TCAATACTACT GGCTGGAAGC CTCTTTACTC  
45201 CTCTGACCAC ACCTGGGATG TCCACCTTGG CCTCTGAGAG TGTGACCTCA  
45251 AGAACAAGTA AGAATAACTT TTTTATTGTG GTAAAATATA AATACTATAA  
45301 AAATTGCCAT TCTAAACATT TTAATTGTAC AACTCAGCAG TACTAATACA  
45351 TTCACATTGT TGTGCAACCC TCACCACTAT CTGTTTTCAA AACTTTTTTT  
45401 ATCACCCCAA ACAGGACTGA AGGAATAATT TCCCATTCCTT CATTCTCCCT  
45451 AGTGCAGTGG TGCAATCTCG GCTCACCACA ACCTCTGAAC CTCTGTCTCC  
45501 TGGGTTCAAG CAATTCTCCT GCATCAGCCT CCTGAGTAGT TGGGACTACA  
45551 GGTGCACGCC ACCGTGCCTG GCTAATTTTT GTATTTTTAG TACAGACAGG  
45601 GTTTTACCAT GTTGGTCAGG CTGGTCTCAA ACTCCTGACC TCAGGTGGTC  
45651 CACACGCCTT GGCCTCCCAA AGTGCTGGGA TTACAAGTGT GAGAACTGT  
45701 GCCCGGCCAT ATCTGTTAGA TCTTACTAAT CCTGTCAAGA GGATTCAGTG

Table 1 (continued)

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**Genomic CA125 Amino Terminal Sequence**  
(SEQ ID NO: 1)

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45751	TCCTTTTTTT	TTTTTCTTTC	TTTTTTTTTGA	TAGAGTCTCC	CTCTGGCACC
45801	CAGGCTGGAG	TGCAGTGGTA	CGGTCTTGGC	TCACTGCAGC	CTCCACCTCC
45851	CAGACTGAAG	CGATTCTCCT	GCCTCAGCCT	CCCGAATAGC	TGGGACTACA
45901	GGCGCGTGCC	ACCACGCCCA	GCTAATTTTT	GCATTTTTAG	TAGAGATGGG
45951	ATTTCACTAT	GTTGGCCAGG	CTGGTCTCAA	ACTCCTGATC	TCAAGTGATC
46001	CGCCCAAGGG	CCTCCCAAAG	TACTGGGATT	ACAGGTAGGA	GCCACCTCAC
46051	CTGGCCCTAT	TTTCGGAATG	GATTTTTTTT	TAATGTTTAA	AATGTCACCT
46101	AAGATTATTG	TGAAGATCAA	ATAAGATAAA	ATCCTAATAA	CCCAAGTAAA
46151	CCACAGGGCT	CCACTTGGAC	CAGTCTCAGA	AGTTTCAAGA	AAATCAGTCA
46201	GACCATCAAA	TGTAAAATAA	GTCTAAATTT	TCTTTGCACT	ATTCACAGAG
46251	TGCCAAAGAG	GATCTAATTC	ATGTTTCAGA	ACATACCCTA	CTTACTAAAA
46301	TCCCCTTTTC	CTCATTTCTT	CTCATTCCTG	AACTTTATCA	TCTCCTGCGG
46351	ACCCCCTAGC	CTCTCCCCTC	CCCATAGTCA	GTCTCTCTCT	CTCTCTTTCC
46401	CTCCCCTCTT	ATTATCTCAA	TTTCACACGA	AAGAATTCCA	GAAACTATAC
46451	TGCCAAAAGT	CTTTCCTGTC	TTTGAAAAGT	TGGGAAAGAG	GAGAAACTCA
46501	GACAGCAATG	ACAAAATTAT	ACGTAATGGA	TGAAGGAAAC	ACAAATAAGG
46551	CTGGAAACAG	AAAATTTTGT	CCCCATCATT	TATTTAATGA	AGGTGGCAGT
46601	ATTCCAGCCA	CATAGTGAAC	CCCCACAATA	AGAAGGGGCC	TCTGGCGATT
46651	GATTATTGTC	ATTGTTGTTA	ATGATAATGA	GGGTGAGGAT	ATCATGAGCA
46701	TCAGTGTAGG	AGGCAGTTAA	CTAATAAGAC	CAAGCTGTTG	GCTGGGCGTG

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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46751 CTGGTTCACA CCTGCAGTCC CAGCACTTTG GGAGGCCAAA GTGGGTGGAT  
 46801 CACTTGAGGT CAGGAGTTCA AGACTAGCCT GGCCAACATG GTGAAACCTG  
 46851 GTCTCTACCA AAAATACAAA AATTAGTCAG GTGTGGTGGC GTGTGCCTGT  
 46901 AATGACAACT ACTTGGGAGG CTGAGGCAGG AGAATCACTT GAACCTGGGA  
 46951 GGCGGAGGCT GCAGTGAGAT GAGCTTGAAC CACTGCACTC CAGCCCGGGC  
 47001 AACAGAGAGA GACTCTTGTC TCAAAAAACA AAACAAACAA ACAAAAACTA  
 47051 AACCAAACAA AAAAAGACTA GCTGTTATTC ATTTATTTAT TTATTTATTT  
 47101 AGAGACGGAG TCTCGCTCTG TCACCCAGGC TGGAGTGCAG CGGCACAATC  
 47151 TTGGCTCACT GCAACCTCTG CCTCCCAGGT TCATGTGATT CTCCCGCCTC  
 47201 AGCCTCCCCA GCTGTTGTTA TTCATGAATG AACCTCAGAG AAAGCACACA  
 47251 GGAGGGTTGG TGCACCTGTG TTTTGAGTTC TACCCCTCCT TCCTCTCTTA  
 47301 ACTTCCTCCT GTCTTCTCAC TCTGATTCTG TCTTCCTTCC TCTCCCTCTC

**Exon 7**

47351 TCTCTGCAGG TTATAACCAT CGGTCCTGGA TCTCCACCAC CAGCAGTGAG  
 47401 TAAACATGGC CCTGAAGTCC CTATGCCCTG GGAATTCTTC CTCCCTAAGC  
 47451 CTGCCTTCCA GGAGGAAAGT ATCCCCCATT CCCTAGGTTC TCATCCCCAC  
 47501 AGAAACTCCA GAATAGCAAA AGTCTCAGGC TGAGCCAAGG CACAGATGCC  
 47551 AGTGCTCACC AAGAGTCCTA TTCTCCCCTC GCTAAATGAT AGGACCCAAC  
 47601 AAACCCGATT CACGCTGCGT TTTCTTTTCTCAG CTCCGATGAC CTCCATGTTC  
 47651 TCTCCAAGGC CTCTCGTATC TGTGAGCCCC ACCCCCAGCG CTACAGGTAG

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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47701 GAATCTGGCT TCCAGCTCCC ATGAAACGTC GGCTGCCATT CAGTGGCTGA  
47751 TTAATTGCTG TGTGGTCTGA GTCCTGATGC CCACCAAGTC TCAGCGTGTT  
47801 CCCCTCTGTC CAATCTCATC CAACAATTTA AGCTAATGCT TGTTTAATGA  
47851 TGTCTCACT ATACCACCTT GGACACTTTC TTTTGCCTG GATTTAAAGC  
47901 TTCCATTTCT TTCCTTCCTT CCTTCTTTTC TTCCTTCCTT CCTTCCTTCC  
47951 TTCCTTCCTT CCTTCCTTCC TTCCTTCCTT CCTTCCTTCC TCCTTCCTTC  
48001 CTTCTTTTCT TCCTTTCTTC CTGTCTTTTT CTTTCTTTCC TTCTTTTGGC  
48051 AGAGTCTCAC TCTGTCGCCC AGGCTGGAGT GCAATGGTGC AATCTCGGTT  
48101 CACTGCAACC TCTGCCTCCC AGGTTCAAGC GATTCTCATG CCACATGCCA  
48151 CTATGCCTGG CTAATTTTTG TTTTTTTGTT TTTTGGGGG TTTTTTGAGA  
48201 CAGAGTCTCA GTCTGTTGCC CAAGCTGGAG TGCAGTGGCA TGATCTCGGG  
48251 TCACTGCAAC CTCCTTCTCC CAGGTTCAAG CGATTTTCCT GCCTCAGCCT  
48301 CCTGAGTAGC TGGAAC TACA GGCACGCACC ATCACACCGG CTAATTTTTT  
48351 GTGTTTTTAG TAGAGACGAC GGTTTTGCAA TGTGGGCCAG GCTTGTCTCG  
48401 AACTCCTGAC CTCAAGTGAT CCTCCAGCCT CGGCCTCTCA AAGTGCTGGG  
48451 ATTACAAGTG TGAGCCACTG CACCAGGCCA AAAACTTGTA TTTCAATAGT  
48501 CATTGAGGCT GGGTGCAGTG GCTCACGCCT GTAATCCCAG CACTTTGGGA  
48551 GGCTGAGGCC AGTGGATCAT GAGGTCAGGA GATCAAGACC ACCCTGGCTA  
48601 ACACAGTGAA ACCCCATCTC TACTAAAAAT ACACACAAAA ATTAGCCGGG  
48651 CATGGTGGCA AGATGCCTGT AGTCCCAGCT ACTCAGGAGG CTGAGGCAGG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
48701	AGAATGGCGT	GAACCTGGGA	GGCAGAGCTT	GCAGTGAGCG	GAGATCGCAC
48751	CGCTGCACTC	CAGCCTGGGC	AACAGAGAGC	GACTCTGTCT	CAAAAAAAAA
48801	AATATATATA	TATATATATA	TATATTCATT	GAGACCGACT	CTGACTTAAA
48851	AGCAGTAATG	AATGGTGTAG	GTTTGGTAA	ATTACAGGTC	TTGCTTTAAG
48901	TCCTGGTCCT	CTCTTTTGCT	CACTGTGTGG	CCCCGGAAGA	GCCATGTAAC
48951	CTCTCCAGGC	TTCAGTGTCC	ATTTT'TAGAA	CGGAGTAAGT	GAATAAGCTG
49001	TGTCCAATCA	TCTCTGGCCA	TATCAGCTTC	ATTTTTTTTT	TCCTCCAGGG
49051	TCCAAACATC	CCTCCACCCT	CAGAGTCTTT	GCACCTGGTG	TTCTTGTCTT
49101	TCAAATCTCA	GCTTGGATCA	CCCTTTATAA	AGTAGCATTT	CCCCCGTATA
49151	CGCATCTTGC	ACACAGCCAA	TCTCTATTCT	ACCTCTATGC	TCACTTCCTT
49201	CCTGGCAATT	ATTACTACAG	CTGGGCCCTT	GAACAGCATG	AGGGTTCAGG
49251	GTGCTGACCC	CTATGCATTC	AAAAATCCAC	ATATAACTTT	TTTTTTTTTG
49301	AGATGGAGTT	TCACACTTGT	TGCCCAGGCT	GGAGTGCACT	GGCGCCATCT
49351	TGGCTCACTG	CAAACCTCTG	CTCCTGGGTT	CAAGTGATTC	TCCTGCCTCA
49401	GCCTCCTGAG	TAGCTGGGAT	TACAGGCATG	TGCCACCATG	CCCAGCTAAT
49451	TTTGTATTTT	TAGTAGAGAT	GAGGTTTCTC	CATGTTGCGC	AGGCTGCTCT
49501	TGAACTCCTG	ACTTCAGGTG	ATCCGCCTGC	CTTGGCCTCC	CAAAGTGCTG
49551	GGATTACAGG	CATGAGCCAT	GATGCCCCGC	CATTTGCTAA	TGGCATCTAG
49601	TAAGTAGAGG	CCAGAGATGT	TGCAAAACAT	CCAACAATGC	ACAAAGCAGC
49651	CTCCTATCAA	AACACATTAT	CCAGACCAAA	ATGTCAATAG	GGCTGAGGTT



Table 1 (continued)

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**Genomic CA125 Amino Terminal Sequence**  
(SEQ ID NO: 1)

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49701 GAGCATCTGC TGTACACAGA TTCCAAGTTC TGGTACAAAT CTCGTAGTTC  
 49751 TCTGAGGGCT CATCTTTCAA TGCCTAGCAC ATCAAAGGAG GCCAATTTCC  
 49801 TCTTCCCTTT CACCTCCTGG TATGAAATGT TTCCTCCTCC ACCTTGATCC  
 49851 TGTAAGAGCC CAGCTGGAGT TTGCAGACGA CGGGGAAAGA AATGGGTGAG  
 49901 GGAGGGTCCT ATGGTTGAGT CTCCGCAGTG GGCCCTGGGT GCCCAGTTCA  
 49951 CCCTCCTCCC CTTCAATTTT TCCATCATGA CAACTCAAGG CAAATTCTCA  
 50001 GTTTCCATGG GCCAGTGGAA TCCACTGACT TCATGAAATA ACCCCACCCT  
 50051 GAGCAAATAC CCCTCAAATA ATAAGTGTTC ACACAACATC AGTGGCAACA  
 50101 ATGACCCAAG CAGCAATGCC ACCACCAGAA TAGCAACCAT AACAGCAGCT  
 50151 CATTTTCATC AAAAGGAAAC TGTAGGGCCA GGCACAGTGG CTCACACCTA  
 50201 TATTCCCAGC ATTTTGGGAG GCTGAGGCAG GCAGATCACC TGAGGTCAGG  
 50251 AGTTCAAGAC CAGCCCAGCC AACATGGTGA AA TCCATCTT CTACTAAAAA  
 50301 TACAAAAACT AGCCAGGCTT GGTGGCATGT GCCTGTAATC CTAGCTACTC  
 50351 GGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CTGGGAGGCA GAGGTTGCAG  
 50401 TGAGCTGAGA TTGTGCCACT GCACTCCAGC CTGGGCGACA GAGCAAGACT  
 50451 CCGTCTGAAA AAAAAAAAAA AAGGAATTGT GCCAGGAATT GTGATGAGAA  
 50501 CTTTATATGC ATTATCTCCT ATTAATATTA CCCAAACCTC CGTGAGTTAC  
 50551 TATACTCATT TCTACAGAGA GCATTTATGC ATCCAGGGAG GAAGTAATTA  
 50601 GCCCAGAATT ACTCAGTTAT GACACAGGAC AGTATGAAAA CTCCAACCGA  
 50651 AGATTGGAGA CTCATGAAAA CTCCAGGCTC CTAAGTACAA GACATCACTG

Table 1 (continued)

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**Genomic CA125 Amino Terminal Sequence**  
(SEQ ID NO: 1)

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50701 TGGATCGTCC AAATAGAGCA AGCCCCAATC TCAGGACAGG AATGAGGCAT  
50751 GAATGGCCTC TATGCTAATG ATCTAACCTA ATGCTGAATT TGTTACTTCC  
50801 CTTCTGAATC CACTTGGAGA TTTCTTTTAT ATCTGACTTG AAATAGAGGA  
50851 TATATACTCC TCTATCCTTG ACATAGGAGA TAATACACAG AAAGTATTTT  
50901 ATTGTAGTAT CAAGTACACA TCCTGTTCTG TGTCCATAGG ATTATGACTA  
50951 ATTTAGGGCA TGGCTTAACA GTGTGGTACT ATTGAATGAC AGACAGATGT  
51001 CTGTTTTGTT GGATGCAGGA CAAGCCATGT AACCTCCCCA GACTTTAGTG  
51051 TCCCCTCTGT GGAATGGAAT AAAAATACTA CGTGGGATTG TTCTGATAAT  
51101 CAAATGAGAT AATTCAGGAA CAACCCAGAT AAATAACAGG GCTGCCCTGG  
51151 GTTCTGTCTT TCCTTGTATC TCTCACAGAG CCTCAAAGGA GATGCAATCC  
51201 ATGACCTAGA GAAACACTCA GGACAAATTC TCTTTTCCCC AGTTCCTTTC  
51251 TTGCTCCAAT GGCAACACCA CCCCTCTCAT CCTGAAGTCT CTTGTTTTTA  
51301 CCACCACACC TATTTTGCCA AATTTTCTCC AATATTCCAA ACCATATGAA  
51351 ACCTTTCTTT CTTTCTTTTC TTTCTTCCT TTCCTTCTTT CTTTCTTTTT  
51401 TCTCTTCTTT TCTTTTCTTT TTGAGACATG GTCTCACTCT GTTGCACAGG  
51451 CTGGAGTGCA ATGGCACGAT CTTTGCTCAC TGCAACCTCC GCCTCCCAGG  
51501 TTCAAGAGAT TCTCTGCCT CAGCCTCCTG AGTAGCTGGG ATTACAGGCG  
51551 CCCACCGCCA CGCCACGCTA ATTTTGTGT TCTTAGTGGA GACGGGGTTT  
51601 CGCCATGTTG GCCAGGCTGG TCTTGAATC CTGACCTCAA GTGATTTGCC  
51651 CATCTCGGTC TCCCAAAGTG CTAGGATTAC AGGCGTGAGC CACCAAGCCC

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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51701 GGCCCCATAT GAACCGTTTC TATCCCTCAT TTCTCTGTAC TTTTACCTAA  
51751 AAACACCACT CCCTTCACCC ATCACATTTT TGTCAATTCT ACATCACACA  
51801 CACACACACA CACACACACA CACACACAGA GAAAGTAAGT TGGAAAAAAA  
51851 TTATACTATC ATGAAATTTT GTGAAAGGAG GTAAGCTGAG AGAGTAAGAA  
51901 TCAAACATAA TTATCTTTAT GGGTAGAAAG CACACTCATC CATACATGTG  
51951 TCTTTCACC CTTGTAATGT ATTTATTATT ATTGTTTGTA TATACTAGAT  
52001 TCCCAATAAA TAGGGACAGC TATTATGGTA TTTTATTTC AGGAATAATA  
52051 ATAGTGATGA TTTCCACCAT TATTGTCAA GGACAAAGCA CAAAATATGT  
52101 ACCAAATAAA ATATAGCCAT TATCCTTTAT TCACAAAAGA TCTTGGCCCC  
52151 ACCTCTTCTC AATGAAATGT CCATGACTTG TTCAACTTTG GCCACTCTGG  
52201 GCTGAGAGAT GGAGGTTCCT TTGCGAGCTG AAGTCACACA TCGAAGGTGG  
52251 AAGCCCCTCC CCTCCCTCTG GCTGGCTGAG GGATAGCCCA GATGGGCTCA  
52301 TCATGAAAGT TTCCATTAT TTCCATTTCT GGATCTACCA TCTTCCCCTC  
52351 CCCTACCTCT CACCCATCAT AATTGTCCTT CTTTACTCTT TCCTCCCTAT

Exon 8

52401 CTGCAGGTTA TAACCGTCGG TACTGGACCC CTGCCACCAG CAGTGAGTAT  
52451 TCAAACCTGT GATATTCCAA TGCCCTTGGG ACCCTTCCTC CCCAAGGTGC  
52501 ATTCCTCAGA AGAGAACTG ATCATTCTCC CTCCCTACGT GCCCAGCCAC  
52551 AGCCTCAGAG CAGCCCCTAA CCCGTCAAGG TCTTGGTGTG AGTCAAGATA  
52601 GAAGTCCAAA TTCCAATGAG CAGTTCCTGT CCCATATTCC TTTAGGAAGA

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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## Exon 9

52651 CACCCAATCA TTTCTCCATG TTCTTTTTTT CTCAGCTCCA GTGACTTCTA  
52701 CATTCTCCCC AGGGATTTC ACATCCTCCA TCCCAGCTC CACAGGTAGG  
52751 AAGCTCCTCT CTGGCATCTA TGAAATTTAA CACTGCATGG TCTGTTCCCT  
52801 GCTGACCACC CAGACTCAGC CTGTTCCACT CGCCCTCTCA CTCTCTCTCT  
52851 CTCTCTTTTT TTTTTTTTTT TTTTTTTTTT TTTACGGAGT CTTGCTCTGT  
52901 CACCCAGGCT GGAGTGGAAT GGTGTGATCT CGGCTCACTG CAACCTTCGC  
52951 CTCCCAGGTT CACGTGATTC TCCTGCCTCA GCCTCCGGAG TAGCTGGGAT  
53001 TACAGGTGCA CACCACCATG CCTGGCTAAT TTTTGTATT TTTAGTAGAG  
53051 ACGGGGTTTC ACCATGTTGG CCAGGCTGGT CTTGAACTCC TGACCTCAAG  
53101 TGATCTACCC ACCTTGGCCT CCCAAAGTGC TGGGATTATA GGCATGAGCC  
53151 ACCACGCCAG GCCCACTCTC TAAATTTTGA CCACCCTGCC TTGAGTGGTC  
53201 TTCTAGCACC CTAACCTCTG TCTAACCTCG AGAGCTTTGC ACTAGCGATT  
53251 CCTGGGGACC AGCTATGGTT GGTATCTTCT CAACTTTCTA ATTTTTTTAA  
53301 AATTATTATT ATTATTATTA TTATTTTAAA TGGAGTCTCG CTCTGTCACC  
53351 CAGGCTGGAG TGCAGTGGCA CCATCTCGGC TCATTGCAAC CTCTACCTCC  
53401 CGGGTTCATG CAATTTTCCT GCCTCAGCCA GAAATTTTCT CAGTGGTCGA  
53451 GATTGTGCCA CTGCACTCCA GCCTGGGCAA TGGAGCTAGG CTCCATCTCA  
53501 AAAAAAAAAA AAAAAAGACG GAGGTCGGGC ATTCTAACC CTTAACCTG  
53551 CCTTGTGATT CTGGAGTTAT GAGATAGAAC CTGGTGTCCC GTAATTAAAA

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
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53601	TTCCGCCTTC	AGGCCTTATG	TTTTGTGAGT	CACAACACTG	CAAACTTTTT
53651	ACATGCTGTA	GACAGGATGT	TCACTCTCCA	CTTCCTCACT	GCTCTGCTCT
53701	AATCAATTCA	ACCATTTATG	TGACATGCCT	AACCCCTCTG	GGCTTGTACG
53751	TATGTAACAT	GTATTACAAA	GCAAGTCATT	CCATGATCAA	TGCTGTCACT
53801	TTTTCTAGGT	GCTTTCAAAA	TTTGTTCTTC	ATCATTGATT	TTCAGTAGTT
53851	TGATTACGAT	GTGTCTGGGC	ATGGTTTTCT	TTGAGTTTAT	CCTGCTTAAA
53901	GTGTTCTCAG	CTTCTTGAGT	CTCAAAGTGT	TTATTTTCTG	CTCTGATTCT
53951	TTCTCCCCTT	CGGACCTCCA	ATGAAATGAT	GTTGCCCGAA	GAGACCCTGA
54001	GGTTCGTTC	ATTTTGTTAT	TTATCAATCT	TTTTTCCTCT	CCGAATTTCA
54051	GGTTTAATAA	TTTTTTTTTT	TTTTTTGAGA	CGGAGTCTCG	CTCTGTCGCC
54101	CAGGCTGGAG	TGCAGTGGCG	CGATCTCGGC	TCACCGCAAG	CTCCGCCCCC
54151	TGGGTTACAG	CCATTCTCCT	GCCTCAGCCT	CCGGAGTAGC	TGGGATTACA
54201	GGCACCCGCC	ACCATGCCCCG	GCTAATTTTT	TGTATTTTTT	AGTAGAGACG
54251	GGGTTTCACC	GTATTAGCCA	GGATGGTCTC	AATCTCCTGA	CCTCGTGATC
54301	CGCCCGCCTC	AGCCTCCTAA	AGAGCTGGGA	TTACAGGCGT	GAGCCACTGC
54351	GCCCGGCCCA	GGTTTAATAA	TTTTTATAGA	ATATTTTCAC	AATCACCAAG
54401	CCTTTTCTCT	ACCAGCTCCA	TTCTGCCCAT	CCATTGAATT	CTTTTTATCT
54451	CAGTTACTTT	ATGTTTCAGT	TCGAAAGTTT	CTACTTGGTT	AGATAGATAG
54501	ATGTTATATC	ATATATTATA	TGTTATATAA	AAATATATTT	ATGGTTATAC
54551	ATATAACATA	TATGTTATAT	ATAGTTATTT	ATATAGCCAT	AACTATATAT

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Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence  
(SEQ ID NO: 1)

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54601 AGCCATATAT ATAGTTATAT ATAACCATAT ATATAGTTAC CATATAGTAA  
54651 CCACATATAT AAAACATATA TATATAGTGT CTCTCTATAT ATAGTTATAT  
54701 ATATAGTTTC TATATCTGTA ACTATATATA GTTATATATG TATGTTTCTC  
54751 TGTATATAAA TATATATATT TCTATATATA TAGTTATACA CATTATATAT  
54801 ATAACTGGGA GATGTTGGTA AAGGATGGCG TGAGGAAACC TGGAGCAGTC  
54851 ATGGTAATCC TCGCTCTGCT CCGAACTCCT CAAGAGCAGG AGAAGGGTCC  
54901 TCCTCATTCT CCAGCCATGT TGACTIONGAG CAATTTACTC ATCCTCTCAG  
54951 TACCTCAGTT TCCTCACCTG CCAATTGAGG ATAATAATAT TTCATAAATT  
55001 GTTTGCAAAT GTTATATGCA ACTCTACGTA AGAACACCTA GCACAGGGGC  
55051 TACCAGGGAA TTTGGTTTAA CAAATATTTA TCAGGCACCT ATTCTGGGCT  
55101 GGGCAGGGGG GATAAGATGT TGACTIONAGTC AAATGCAGTC CCTCCCCTCA  
55151 CCAAGTTTAC AGTGTATTGG GCAAGACTGA AATGGAACAA GCAATTACAA  
55201 TTGACAATAA AAGACAACCA AGTTATTGAG CACTTACTAT ATGGCATGCC  
55251 ATATGCTATG TATTTTTTTT ATTTTAACT TTTCAATTTG AAATAAATAA  
55301 TAAATATAAA GTAAATAATA ATATAAATAA ATAATAAATA ACTTTTCATT  
55351 TTGAAATAAA TAATAAATAA ATTCAGGAGA TGTTGCGAAA ATAGTGTAGC  
55401 ATTCCCCTGT ATCCTTCACC CAGTTTCTCC CCAATGGCTA CATCTTACAT  
55451 AACTCTAATA CAATATCAAA AGCAGGAAAC TGACATTGTT AAAATCCATT  
55501 TTACTIONGTTT TACACGCGTG TGTGCATATG TGAGCTTG TG TATGTGCGTG  
55551 TGTGTGCAGG CATGTGTGTG CATGCACGCC TGTGTGTGCA TATGTGCATG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
55601	TGTGCATGCG	TGTGTGCATG	TGTGCATGTG	TGTGTGCATG	CGTGCGTGCG
55651	TGCGTGCATC	TGTGTGCATG	TATGCACATG	TGTGTGTGTC	TGTGCACGTG
55701	TGTGCATGCA	TGTGTGTGTG	CGTGTGTGTT	GGTAGCCCTA	TGCAATTTTT
55751	ATCACATGGG	CATAGCCCTA	TAATCACCAC	CACCATCAAG	ATTCAGAACT
55801	GTTCCATTCC	CCCAAAGATT	CCCCTCATGC	TAGCCTTCGT	AATCATGCCC
55851	ACTGAGCCCA	ACACTATTGC	ATAGAATAGC	TATTCTACTC	TCCATCTCCA
55901	TCTCTGTCTC	TACAATTTTC	TTTTGAAGAT	GTTATATAAA	TGGAAATGTA
55951	CAACATGTCA	CCTTTGAAAT	TGGCTTCTTT	TCCACTCAGT	GTAATGCCCT
56001	GGAGATGTGC	TCTTTTAAAC	AGTCATGTAA	CCTTCCTAAT	TTCCCTCCAA
56051	AATATCATTA	TGCCCCTCGC	CGCCTTTTTT	TTTTTTTTTT	TTTTTTGAGA
56101	CAGAGTCTCG	CTCTGTTGCC	CAGGCTGGAG	TGCAGTGGTA	TAATCTCAGC
56151	TCACTGCAGC	CTCCGTCTCC	CGGGTTCAAG	GGATTCCCCT	GCCTCAGCCT
56201	CCCAAGTAGC	CAGGATTACA	AGTGCATGCC	ACCACGCCTG	GCTAATTTTT
56251	GTATTTTTAG	TCGAGACGGG	GTTTCATTGT	GTTGGCCAGG	CTGGTCTCGA
56301	ATTCCTGACC	TCAAGTGATC	TGCCCCCCTT	GGCCTCCCAA	AGTGCTGGGA
56351	TTACAGGTGT	GAGCCACCGC	GCCCGACCCA	TATTGCCCAT	TGTATTACAG
56401	CGGAAGAAAC	TGAGGTATGG	ACAGGTAACA	TGTCCATGGT	CACTTGGCTG
56451	GTGAGGGGCA	GAGAGGAGAT	TTGAAACCAA	ATCTGACTCA	CTAGTGTGGC
56501	CGTAACCATG	GTAACATATG	CTCTCTACCA	TGTGGTCTCC	TCTTTATTAA
56551	AGGAAGGGCA	AGTTCTGGGA	GTTTTGGGAG	TTTTGGGCTT	GAGTGGGGAA

Table 1 (continued)

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Genomic CA125 Amino Terminal Sequence	
(SEQ ID NO: 1)	

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56601	GGGTAGCCAA GTAAAGCAGG TGAGAGAAGG TCTGCTTTAA GGACTGCTGT
56651	TTGATTTTAA TTGTTGTTGT TCAGTGTTCA ATGGGATTGA GTTGACTCTT
56701	TTTTCCCTTC TTGTTCCCA AAGCATGAGA CTGTTCCGGT CCTTTTCCCT
56751	TTTAACTTCT CAGCTAGAGT TTGTTAGGGC GGGTATGGGC ACCTGGCAGA
56801	GTCTGAGACC TCAGCTTCCA GTAGGCACAC GTTCTGACCC AATACACCTA
56851	CCCTGGTCCC CTAACCTGCT TCTGGTCCCC TAACCTGCTT CTGGGCCCAG
56901	GTAATGCATT TTAGGAACAT CCCACTTTTC TCCTTACCTG GCTTTCCATT
56951	ATCCGTCCAA ACTAAAGCAC CCACCTGTCT GCTTCAGACT CTTGCTTCAA
57001	GCACTCCGTC TGGGTCCTCA GAAATTGACT TACAGTCAGT TCAGATCTGA
57051	CTCAGGCGTG GCCTTCTTTT CTCCTTCCTT GC



Table 2

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**Genomic Repeats  
(SEQ ID NO: 2)**

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**ExonR1**

1 AGCAGCCACA GTCCCATTTCA TGGTGCCATT CACCCTCAAC TTCACCATCA  
51 CCAACCTGCA GTACGAGGAG GACATGCGGC ACCCTGGTTC CAGGAAGTTC  
101 AACGCCACAG AGAGAGAACT GCAGGGTCTG GTGAGAGCCC CGCCCACCGT  
151 ACTCCTCCCT CGCCCACCTTA GACAAACCAG CCCACCTCAC ACTGCCTCGC  
201 CCACTGATGC CAGCCACGCC CACCTCATCC AACCCAGAC ACCTTTCCCT  
251 GCCCCACCCA CTGATTTTAG CCAAGCCCAC CTCACCCAC CCAGCCTACT  
301 GATGCCAGCC ACGCCACCT TTCCCTGCCC CGCCCACTGA TTTCAGCCAC  
351 GCCCACCTCA CCCTGGTCCA CCCCTCCAAT GCCCACTCT TCCTGGCTTC

**Exon R2**

401 CCGCAGCTGT TGTTTCTCAC CTCCCCTCTC CTTCTTGCA GCTCAAACCC  
451 TTGTTCAGGA ATAGCAGTCT GGAATACCTC TATTCAGGCT GCAGACTAGC  
501 CTCACTCAGG TGAGACGCTC CTTAAGAAAA ACACAGCCCA ACAGGTGAAT  
551 ATGACCCTAG TCTCTGGGCT CCCTGACTCT GTTCATACTT GGAACAACCTA  
601 TTGCCCATGG ATACTAAGCA TCACCACCAG CAGCAGCAGA TAACTATTCC  
651 TAAGACCCAA GGCACATGCAT TATGTACTTT ATATTTAATG CCTCATCAGT  
701 GCTTGCAACA GCCTCATGAA GCAGGAGCAG AAGGGGAAAC TGAGGCCAG  
751 ATTAAGTGGC TTGTGCCAGG ACACACAAAG CAACTGCAGC ACTTCAGGTT  
801 CTATATCCAA ACTCCTATCC CTTAGGTGGC ACTTCCTCCT CTGCCCCCAT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
851	TATGAACTTG	CAGCATGTGG	AAAACCCCAA	TCTGACTTCC	CTCTAAGGGA
901	ACTTGCCCAG	AGAATCTAAG	AGGGGAGGAA	AGGAAGGCGT	TCAGCCCTTA
951	CAGGCAGGAG	GTCAGCTCCT	GAGTGGCTCA	GATGCAGCCA	CAGAGGGCCT
1001	GGCCGGTCTG	AGGGTGACTG	AGAGGCACCG	AGGGCACTGT	CCCTGAGTGC
1051	TGGAAAGGGC	AGGTCTTTTA	GGGTAGACAG	CGGTTGATAT	CATTTCTCTG
1101	CTGGCATTCT	CACCTTCCAC	ACCTCTCTCA	CAGAATCTCC	AAGTGTGGCT
1151	CTCCCAAGAG	AGAGTGTGAG	TCATCTACCT	CCAGCTTCCT	TTCTTCCCA
1201	GGGGGAAGAG	GGGACAGGGG	GGCCCTAGTG	GCTAAGAGCA	TTGGTGAACT
1251	CAGGCAGACC	TCAGTTCTGA	ACCAACCCAG	CTCTGCCATT	TACTATCTGT
1301	GACTCTGAGC	AAGTGCCTGA	AGCCTTCTGT	GCCCTATTTC	CTGACATATT
1351	ATATATATAA	AATACATATA	TTATATATAG	ACATATTTTA	TATACATATT
1401	GAGGCATATT	TTATAACAT	GTTTATAGAC	ACATTTTAT	ATGCATATGT
1451	TATATACGTA	TATAACATAT	GTTATATATA	ATGTATATAT	TATACATATT
1501	GTTATATTGT	ATACATGTTA	TATATGTTAT	AGCATATATA	GTACAAGTTA
1551	TATATAACAC	ATACATTATG	TTACATATAA	TGTATATGTT	ATATATGATA
1601	TATTATATAT	AATTATATAT	TATATAAAAC	TGTTATATAT	AATTATATAT
1651	AATATATAGT	TGTTATATAT	AATTATATAA	TTGTTATATA	TTATATACAA
1701	CATATAACAT	ACATTATATA	TTGTTATATA	TAATATAATA	TATACATATA
1751	TAACATATGT	ATAACTTTTA	TGTTATACAT	AATGTATATA	ACATATATGT
1801	GATGTGTGA	TGTACATAAC	ATATCTGACA	TTAACATATA	ACATATGATA
1851	TAACAATATT	ATATGTTATA	ACATAATATA	TGTTATAATA	TAACAATATT
1901	ATATGTTATA	ACTTATACTG	TCATATGTAA	CATATACATA	ATATTTTATA

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
1951	AATCAGTTTA	ATATACATTA	TGTTACATAT	AATGTATGTT	ATATATGATA
2001	TATTATATAT	AATTATATTA	TACATAATTG	TTATATATAA	TGCATACATT
2051	GTATTTGTTA	CGTATTATAT	GCAACATATG	GGGATCCTCT	AGAGTCGGAC
2101	CAGCGGCAGC	AGCTGCCTGC	CTTTTNNNNN	NNNNNNNNNN	NNNNNNNNNN
2151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
2201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
2251	ATATACATAC	ATAACATATG	TATAACTTAT	ATGTTATATA	TAAGTATATA
2301	ACATATATGT	GTATGTGATG	TATATAACAT	ATCTGACATT	AACATATAAC
2351	ATATGTTATA	ATATGACATA	TTATATATAT	TACATATAAC	GTATATCATG
2401	TATAATATAA	TGTGTATATA	TAATATATTA	AAGTATATAA	GTATAAATAC
2451	ATGTAATATT	TAAATATATA	TTATATATAG	TATACATGTG	GATACATACA
2501	ACTTCTACAT	ATACCTAGTA	TATATTCTAT	ATATAAACAG	TCCATGAATT
2551	ACAATGATTC	AACCTATGAT	TTTTCAAAC	TTGTGATAAT	GCCATAGCAA
2601	TATGCATTCA	GTAGAAAGCA	TACCTTCAAC	ACCCATGCAA	CCATTCTGTC
2651	ATTCAC TTTC	AGTACAATAT	TCAATAAATT	ATATGAGATA	TTCAACAGTT
2701	TATTATAAAA	TAGGCTTTGT	GTTAGGTGAT	TTTGCCCACA	TGTAGGCTAA
2751	TGTAAGGGTT	CAGAGCATGT	TTAAGGTAGG	ATAGGCTAAC	CTATCATGTT
2801	CTGTAGGTTA	GGTATAGTCG	ATTTT TATTT	TTATTTT TAT	TTTTGAGACA
2851	GAGTCTTGCT	CTGTCACCCA	GACTGGAATG	CACTGGTGCG	ATCATAGCTC
2901	ACTGCAGCCT	TGAACTCCTG	GGCTCAAGTG	ATCCTCCTAC	CTCAGCCTCC
2951	TGAGTAGCTG	GGACTACAGG	TGTGTGCCAC	CACACCTGGC	TATTTTTTTT
3001	TTAATTTTTT	TTTTTTTGTG	GAGAGGAGGG	TCTTGCCATG	TTGCCCAGGT
3051	GGCCTTGAAC	TCCTGGGCTC	AAGGAATCCT	CCCACCTTGG	CCTCCCAAAA
3101	TCCTGGGATT	ACAGGTGTGA	GCCATCACGC	CCGGCTACAG	GGCATT TTTT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
3151	ACTTATGACA	TTTTCAGTTC	ACAATGGATT	TGTCAGGGCT	GGGCATGATG
3201	GCTCACACCT	GTCATCCCAG	CACTTTGGGA	GGCTGAGGCA	GGTGGATCAC
3251	TTGAGGCCAG	GAGTTTGAGA	CCAGGCTGTC	CAAATGGCAA	AATCTTGTCT
3301	CTACTAAAAA	TACAAAAATT	AGCCAGGCGT	GGTGTGACAA	CTGTAGTTCC
3351	AGCTACTCGG	GAGACTGAAG	CGTGAGAATC	ACTTGAACCT	AGGAGATGGA
3401	AGTTACAGTG	AGTCAAGATC	ACACCACCGC	ACTCCAGCCT	GGATGACAGA
3451	GCAAGACTCT	TGTCCTCCAA	AAACAAAAAA	CAGGCTGGGT	GCATGGCTCA
3501	TGCCTGTAAT	CCCAGCAGTT	TGGGAAGCTG	AGGCAGGTTT	ATCACCTGAG
3551	GTCAGTAGTT	CACGATCAGC	TTGGCAAACA	TGGAGAAAAC	CCATCTCTAC
3601	TAAAAATACA	AAAATTAGCT	GGATGTGGTG	GTGGGTACCT	GTAGTCCCAG
3651	CTACTCGGGA	GGCTGAGGCA	GGAGAATGGA	TTGAACCTGG	GAGGCAGAGG
3701	TTGCAGTGAG	CCAAGATCAC	ACCATTTAAC	TCCAGCCTGG	GCAACAGAGT
3751	GAGACTCCAT	CTCCAAAAAC	AAAAGAAAGC	AAAAACAAAA	AAATAAAATA
3801	AAAAACCTGT	GTTTATCAGG	ACATAATACC	ATCATGAGTC	AAGAAGCATC
3851	TAAATGTACA	TGGTAGTTAT	ATAAAAATAG	TTATATAGTT	ATATACAATA
3901	GTTATATATA	AACCAGTTTA	ATATATGTTA	AGTAGAGGTA	TATGGTAGTT
3951	ATATAAAAAA	TAGTTATATA	ATAGTTATAG	AGTTATATAA	TTATATAAAA
4001	TAGTTATATA	TAAACCAGTT	TAATATATGT	TAGGTAGAGG	TATAATAATA
4051	TATATTGTAT	ATACTATATA	ATATAGTAAT	GTATAAAATG	CAAAACGATA
4101	TCATATATTT	CTATATTAAG	TTTATATTTA	CAGATCTACA	TTTTATATAT
4151	TTTATGTTAT	ATACAATTGT	GTTATACATA	ATATAATTAG	TATAGTACTG
4201	ACTTGGGGAA	TTGAGCAGTA	CCAACCCATA	GGGATGTTTG	AGGATGAAAA
4251	TATGTGATTA	TGAATACAAA	ATGCTGGGCC	TGCTGCATAG	GAAGTATTTA
4301	ATAAATGGTA	GTTGTTACTA	TAAAGTCGTT	CCTACTATAG	AGCTACTCAC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
4351	AACCTGGGAC	ATAGGGAAAG	AGCCCCGTTTC	CCTCTAATCA	CTCAATAGTG
4401	GGTGGCTAGG	TAGGTGAGTC	CACATCCTGT	GGCCGGGAAC	AGGTGCTGAG
4451	ACATGAAGAC	CTTCTGACTG	CATGTTGGAC	CAGCCACAGT	TTCAGACGGA
4501	CCAGCCAAAA	AGGGCATTTC	CCCCAAGCCA	TTTAGCTCCC	TTGAGTCTCA
4551	TAACAAATCT	CCTAGACCCT	GCTGGTCCAT	AGGATCTAGA	GAGGATGACT
4601	TGAACCTTCT	GATCCCACCA	TTTGAAAACG	CCATGCCATG	GGCACCAGTA
4651	GGAGGGCCAC	TGCTACGTGC	ACCAGTACAA	GGGCCACTGC	CATGGATTAC
4701	AGATTAACCC	TAAGTATAGC	TGTCGCACAC	CTAGTACTTC	AGGAGGCTTA
4751	TTCGGGGCCA	TGCAGATCCC	TGGCATTATT	ATCCTAGGAT	CCTACACCAA
4801	GCAAAGCAGG	AGCTGCCCCCT	CCTCATAAAC	CCATAAGCCC	TCCTCTTGAG
4851	CAAAGCAGCT	GGGAAGGCCA	GAAGTTATTC	AAGCTCCCCCT	CTGCCCCGGT
4901	TCCAAAGACA	GACAGCTCAA	GCCTACATGC	AGCAAACCCT	ATAAAAGTGT
4951	CACCTCTTGG	CATTTCTGCC	ATGGTAATGC	TTTCTGCTTC	CACTAATAAT
5001	CCTAGTAATT	TGTTTATGGT	GGGCATCTCT	CTGATGAGAA	CCACATTCTT
5051	TTTTTTTTTT	TTTTTTTTTT	TTGAGATAGA	GTCTCACTCT	GTTGCCCAGA
5101	CTGGAGTGCA	GTGGCGCGAT	CTCGGCTCAC	TGTAACCTTT	GGCTCCTAGG
5151	TTCAAGCAAT	TCTCCTGCCT	CAGCCTCCCA	AGTAGCTGGG	ACTGCAGGCA
5201	CGTACCACCA	TGCCCAGCTA	ATTTTTGTAT	TTTLAGTTGA	GACGGGGTTT
5251	CACCATGTTA	GCCAGGATGG	TCTCAATCTC	TTGACCTCAT	GATCCACCTG
5301	CCTTGGCCTC	CCAAAGTGTT	GGGATTACAG	GCATGAGCCA	CCATGCCTAG
5351	CCTGAGAGCC	ACATTCTTGT	TAACCACAAT	TTTCTCAGAG	TCTGCATTAG
5401	GGGTTGACAA	AGAGTGGAAG	GGAAGGACAA	AAGGATGGAG	AGGTGGATGG

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**


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**Exon R3**

5451 ACTAAGCATA TGTAGGTTCT TACCCAGGCC AGAGAAGGAT AGCTCAGCCA  
 5501 CGGCAGTGGA TGCCATCTGC ACACATCGCC CTGACCCTGA AGACCTCGGA  
 5551 CTGGACAGAG AGCGACTGTA CTGGGAGCTG AGCAATCTGA CAAATGGCAT  
 5601 CCAGGAGCTG GGCCCCTACA CCCTGGACCG GAACAGTCTC TATGTCAATG  
 5651 GTGAGCAGCT GTGATGTGGT TGGAGGCTCT TCCTCCTTGC TGAGCAGCCT  
 5701 GTAATCACTG GCTTGAGGTC AACTCACTG TCAGGCAATT GAAAATTTGG  
 5751 TCCTGTGCTC TACATGGGAT GACTAATTTT CGGACTTCAT GGTATCTTTT  
 5801 TTTTTTTTTT TTTTTTTTTG AGATGGAGTC TCGCTCTGTC ACCAGGCTGA  
 5851 GGTGCAGTGG CATGATCTCA GCTCACTGCA ACCTCCGCCT CCCGGATTCA  
 5901 AGCAATTCTC CTGCCTCAGC CTCCTGAGTA GCTGGGACTA CAGGTGCATG  
 5951 CCACCACACC CAGCTAATTT TTGTATTTTT AGTAGAGACA GGGTTTCACC  
 6001 ATGTTGGTCA GGATGGTCTC AATCTCTTGA CCTTCTACTC CACCTTGCCCT  
 6051 TGGCCTCCCA AAGTACTGGG ATTACAGGCT TGAGCCACCA CACCTGGCCA  
 6101 GGACTTCATG GTTCTTCAT CATCATGGAA TGAATTCCAT CAGGGCATTC  
 6151 TTCCCTGATG TGAGGGCACT GATAGGAAAT CTTTAATGGT CCCTGCTGCA  
 6201 TGAAACTGCT TCCATTGCAC CAGGGTAGCC CTGACCCCTA TTTGGTCCCC  
 6251 CACATCTCCT TGTAACCTAC CCACACTCCT CCCTCCTTCT CTGTGCAGGT

**Exon R4**

6301 TTCACCCATC GAAGCTCTAT GCCCACCACC AGCAGTGAGT ATTCAACTCA  
 6351 TGTCCACATG CCCATGATCC TACACCAAGC AAAGCAGGAG CTGCCCCCTCC  
 6401 TCATAAACCC ATAAGTCCTC CTCTTGAGCA AAGTAGCTGG GAAGGCAGAA  
 6451 GTTATTCAAG CTCCCCCTCTG CCCCAGTTTC AAAGACAGAC TCAGCTCAAG  
 6501 CCCACATGCA GCAAACCCTA TAAAAGTCTC ACCTCTTGGC ATTTCTGCCA

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**

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6551 TGGTAATGCT TTCTGCTCTC ACTAATGAGG ACTTCTCCTC AGCTCCTGGG

**Exon R5**

6601 ACCTCCACAG TGGATGTGGG AACCTCAGGG ACTCCATCCT CCAGCCCCAG  
6651 CCCCACGAGT AAGTACCAGT CAATGGCATC TCTATTAGAG CATGCTATCT  
6701 CTGTCATTTT TACTCAGATG AAGATGGAAA ATCATAGCAA ATCTACTGAT  
6751 AGTGAGTGGA CCAACGAAAT TTGTTGGCCA CCTAGTGTGT ACCAGATCCT  
6801 AGAGATACAG GAGGGAAAAC AAAACCAATA CAAAATTTCT GCTCTCAGTG  
6851 AGCTTGTATT CTTGTCATGA TGATGATGTT GGTGGTGGTG CTGTTGATGA  
6901 CGATGATGAT GATGATGATG ATGATGATGC TGGTGATACT GTTGATGGTG  
6951 ATAGTGATGT TGATGACAAT GATGATGATG ATGATGTTGA AGAAAATGAT  
7001 GCTGGTGATG GTGGTGGGGG TTATTATGGT AATAATGATA TGTTGAGTGT  
7051 GACGATGATG GTGGTGGTGT TGATGATGAT GATGATTATT ATGCTAGTGA  
7101 CATTGATGAT GGTAAATGGTG ATATCAACGA CAGTGACAAT GATGGTGATG  
7151 AGGATGATGT CGGTGATGGT GGTGGGGTTA TGATGGTAAT GATATGTTGA  
7201 ATGTGATGAT GGTGATGATG ATATTTGTGG TTCATGATGG GGATTGTCAT  
7251 GGTGGTGCTG GTGGTACTTG TGATGACAAT AATGATAATA ATGATGACAA  
7301 TGATAGTGAT GATGGTGATG GTGATAATAA AGATAACAGA TATCACCTTA  
7351 CAATATTGAG CACTAAATAT GTACCAAGAG CTATGCTCAG TATCTAACTA  
7401 CTATTATATA ATCTACTTTA GAAAATGAAT TGTATCATAG ATAAGAAAGG

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**

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7451 CGTGGAAAAT ATTTATTATG TCACTCAATT TAATTGCTGC ATATGGTTAT

7501 TACAAAGTGC TATTCTCTCT ACTTTGAACA TAATGTTTAT TTCACACTCC

**Exon R1**

7551 CACTATAGCT GCTGGCCCTC TCCTGATGCC GTTCACCCTC AACTTCACCA

7601 TCACCAACCT GCAGTACGAG GAGGACATGC GTCGCACTGG CTCCAGGAAG

7651 TTCAACACCA TGGAGAGTGT CCTGCAGGGT CTGGTTAGTG TCCTGCCCTC

7701 CACACTCTGC CCTGCTCATG ATACCCAGTC CCTCTTACAT CATCCATGCC

7751 AGGGCAATGG AAGAATATCA AACCCAACTC ACTTTTGCCC CAAGAGATGC

7801 AAGCCTCAGC CAGGAGCGGT GGCTCACGCC TGTAATACCA GCATTTGGGA

7851 GGCCAAGGCG GGTGGATCAC CTGAGGTCAG GAGTTTGTGA CCAGCCTGGC

7901 CAACATAGTG AAACCTCATC CCTACTAAAA TACAAAAATT AGCCAAGCAT

7951 GGTGGTGCAT GCCTGTAATC CCAGCTACTT GGGAGGGTGA GGCAAGAGAA

8001 TCACTTGAAT CAAGGAGGCA GAGGTTGCAG TGAGTCAAGA TCATGCCACT

8051 TTACTCCAGC CTAGGCAAAA AAGCGAACT CCATCTCACA AAAAAAAGAA

8101 AAAAAGAGAG AGATGCAAGC CTCCCCACC AAGGCCAGCC CTGCCCACCT

8151 CACTTCTGCC TGGCTCTTAC ATAAAACTTA GCCCTCCTAC TCACTGCCCT

**Exon R2**

8201 CTCCCTCCTC CACAGCTCAA GCCCTTGTTT AAGAACACCA GTGTTGGCCC

8251 TCTGTACTCT GGCTGCAGAT TGACCTTGCT CAGGTGAGAA CTTAGAATTT

8301 CCAGCCTGGC TGCCCCACTT GTACTCACTC CAAAAGACTT TGCACTGCTT



Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
8351	CCTTGCTGCA	CTTCCTAGGG	ATATCCTCAC	CAAAGGTGGA	ATTCAGGAGT
8401	CACAGGCTTC	AGGATCAGTG	TGTTTCCTGA	CAGTAACACC	CCTACACTCC
8451	ACCTCAACAG	AGAGAATCTG	CATGGCCCAT	CATCAGGATT	GAGCCTCTCC
8501	CTTTATCATC	CCTCTGAATT	CCCTCCATTC	CCTGTGCCTC	CCTTTCCTTT
8551	ACATGTTAAA	TTCTGTCCCC	AGGATTTCTT	TCAGGACAAAT	CATGCCTTAT
8601	CCACGTGATT	TCATCCTCAT	TTCGAGCTCT	TCACTGGGCT	CAAGTCCGGC
8651	TCCCCGTCCC	GTCCATGAAA	GTGTCAGTTT	CATCTTGTC	CTGTATCCGT
8701	GACTCCACTC	ACAGTCCTCA	GCAAGCCAAT	AGTCCATGCA	CTAAGAGTCG
8751	ATGTGGCTTC	TCACCTCTTT	CCCAGGTTTC	TCATTTCTCT	GGTCCTTGCT
8801	GTCCTTCCCT	CAGCAATCGC	AAGACCCTTC	CTAGATAAAC	TTTTCATTGT

**Exon R3**

8851	GATTTTCCC	ACTGACCCTC	CCCAGGCCCG	AGAAAGATGG	GGCAGCCACT
8901	GGAGTGGATG	CCATCTGCAC	CCACCGCCTT	GACCCCAAAA	GCCCTGGACT
8951	CAACAGGGAG	CAGCTGTACT	GGGAGCTAAG	CAATGACC	AATGACATTG
9001	AAGAGCTGGG	CCCCTACACC	CTGGACAGGA	ACAGTCTCTA	TGTCAATGGT
9051	GAGTGGCTGT	GATGTGGTTG	AAATCTCTTC	CCCCTTGCTG	GGCAGCCTCT
9101	AATCTCTAAC	TAGAGATCAC	ACTCCCTGCC	TGGCCTTTGA	AAATTCTGTC
9151	ATGTGCTCTA	CATGGGATGA	CTAAGGTCTG	GACTTCATGG	TTTCCTTACC
9201	ATCATGGACT	GTGTTCCCTC	AGGGCATTCT	TTCCTGATGT	GAGGATGCTG
9251	ATAGAAAATC	TTCAATTGTC	CCTGTACCAT	GAAACTCGGT	TCATTGCACC
9301	AGGGTAGCAT	TGACCTCCAT	TTGGTCCCCC	ACCTCTCCTT	GTCTCTTACC

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**


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**Exon R4**

9351 CACTCTCCTC CCTCCTTCTC TATGCAGGTT TCACCCATCA GAGCTCTGTG  
 9401 TCCACCACCA GCAGTGAGTA TTCAACTCAT ATCCACATGC CTCGGTTCCT  
 9451 ACACCAAGAG GAGCAGGAGC TGGCCCCCTCC TCATAAACCC ATTAAGTCCT  
 9501 CTTCATAAGC AAAGGATTTA GGAGGGCAGA AGTTATTTAA GTGTCCCTCT  
 9551 GCCCAGCTCA AGAGACCGAC CCAGCTCAAG CTACACATGC AACAAACCCC  
 9601 ATAAATAGTC TCCCCTCTTG CCATTTCTGC CAAGAGAGTG CTTTATGCTT

**Exon R5**

9651 TCACTGATGA GAACTTTTCC TCAGCTCCTG GGACCTCCAC AGTGGATCTC  
 9701 AGAACCTCAG GGACTCCATC CTCCTCTCTC AGCCCCACAA GTAAGTATCA  
 9751 GTCAATGACA TCTCTATGAG AGCATACCTG ATTAGTGTA ACATCTCTGT  
 9801 CATTTTCACT CAAATAAAGA TGGAAAATCA TAGTAAATCT AGTGATACTG  
 9851 AGTGGACAAA TTTGTTTGTT TGTTTTTTCT CATCCTTTTC ACTTTTTTTA  
 9901 TTATACTTTA AGTTTtaggg TACATGTGCA CAATGTGCAG TTTAGTTACA  
 9951 CATGTATACA TGTGCCATGC TGGTGTGCTG CACCCATTTG CTCGTCATTT  
 10001 AGCATTAAAGT ATATGTCCTA TGCGATCCAA GCCCACGCGC CGCACCACGT  
 10051 GCAACAGTTT CACAGATTGG ATGGTCCGAT ANNNNNNNNN NNNNNNNNNN  
 10101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
 10151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**

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**Exon R1**

10201 CTTCACCATC ACCAACCTGC AGTATGAGGA GGACATGCAT CGCCCTGGAT  
10251 CTAGGAAGTT CAACACCACA GAGAGGGTCC TGCAGGGTCT GGTAGCACC  
10301 CTGCCCTCTT CACTCTCCCC CGCCCTGGAT GCCGAGCCCC TCATACAACA  
10351 TTCATGCCAG GGCAATGGAA GAATATCGCA CCAACCTTGC CCTCATCCCC  
10401 AGAGATGCAA GCCTCACCCA CTGAGGCCAG CCACTCTCAT GGGTGTCTGC  
10451 CCCACCCACC TCACTTTTGT CCCACACAG GGACCTTAGC CCTCCTACTT

**Exon R2**

10501 ACCTCTCTCT CCCTCCCCCA CAGCTTAGTC CCATATTCAA GAACACCAGT  
10551 GTTGGCCCTC TGTACTCTGG CTGCAGACTG ACCTCTCTCA GGTGAGACCT  
10601 TAGAAGATCC AGCCTGGCTG CCCAGTTGT TCCCACTCCA GTAGATTTTG  
10651 CTCTGCTTCC TTGCTGCACC TCCTAGGGAT ATCCTCACCA AAAGGGGAAT  
10701 TCAGGAGTCA CTGGCTTCTG GACCAATGTG TTTCTGATA GTAACACTCC  
10751 CACACCTCAC CTCAACAGGG AGAATCTGCA TGGTCCATCA TCAGGATTGA  
10801 GCCTCTATCC TGATCATCCC TCAGAATTCC CTGCCCCCTCC CTTTCATTTA  
10851 GGTGTTAAAT TCTGTCCCCA GAATTTCTCT CAAGACAATC ATGCCTCATC  
10901 CAAGTGCTTT CATCCCTGTT TCTAGCTCTT CACTGGTCTC AAGTCTGGGC  
10951 TCTCCTGTCC CCATGCTATG AGAATGCAGG TTTCACCTTG CACTTTTATA  
11001 AGCATGGTTG TATCTGTGAC TCTGTGCACA GTCCCAAGCA AGCCAGTAGT  
11051 CCATGCACTC AGAGAATCTA AGTGTAGCTT CTCACCTCTT TCCCAGGTTT  
11101 CTCATTTCTT CTGGTTCTTT ACTGTCTTTC CATCAGCAGT CTCAGGACAC

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**

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**Exon R3**

11151 AACCTAAGTA ATCTTTTCAT AGTCATTCTC CCCACCTACC TTCCCAGGT  
 11201 CTGAGAAGGA TGGAGCAGCC ACTGGAGTGG ATGCCATCTG CATCCATCAT  
 11251 CTTGACCCCA AAAGCCCTGG ACTCAACAGA GAGCGGCTGT ACTGGGAGCT  
 11301 GAGCCGACTG ACCAATGGCA TCAAAGAGCT GGGCCCCTAC ACCCTGGACA  
 11351 GGAACAGTCT CTATGTCAAT GGTGAGCAGC TGTGATGTGG TTGGAGTCTT  
 11401 TTCCTTCTAG AGTCTGGAAA GAATCTAATC TGTGGCTTGA AGTCACACTC  
 11451 CCTGCCTGGC CATTGAATAT TCTGTCATGT GGTGTAGATG GGATGACAAA  
 11501 GTTCTGGACT TCACAGTTTC TTCATTGTCG TGAAGTGTGT TCCCTCAGGG  
 11551 CACTCTTCCC TGTGTGAGG ATACTGATAG GAATTCTTTA ATGGCCCCAG  
 11601 TCCCATGAAA CTCATTGTCC CATGAAACTC ATTTAATTGC ATTGGGATTG  
 11651 CCATGACCTT ATTGTGTCCC TCGTATCTCC TTAACGCTTA CCAAGTCTCC

**Exon R4**

11701 TCCCTCCTTC TCTATGCAGG TTTCACCCAT CGGACCTCTG TGCCCACCAC  
 11751 CAGCAGTGAG TATTCAACTC ATGTCCACAT GCCCCTGATC CTACATTAAG  
 11801 TGGAGCAGGA GCTGGCCCCCT CCTCTTAAAC CCATAAGTCC TCCTCTTGAG  
 11851 CAAAGGAGCT GGAAGGCAG AAGTTATTGA AGCTCCCTTC CACCTAGCTC  
 11901 CAAAGACAGG CCCAGCTCAT GCCCGTATGC AGCAGACCTC ATAATAGTCT  
 11951 ACCTTCTTGC CATTTCTGCC ATGAGATTAT TTTCTGCTTT CACTGATGAG

**Exon R5**

12001 CACTTTTTCT CAGCTCCTGG GACCTCCACA GTGGACNNNN NNNNNNNNNN  
 12051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
 12101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**

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**Exon R1**

12151 ATTTTCAATT CCCACTACAG CTGCTGGCCC TCTCCTGGTG CTGTTCACCC  
12201 TCAACTTCAC CATCACCAAC CTGAAGTATG AGGAGGACAT GCATCGCCCT  
12251 GGCTCCAGGA AGTTCAACAC CACTGAGAGG GTCCTGCAGA CTCTGGTTAG  
12301 TGCCCTTCCC TCCTCACTCT GCCCAGCCCC AGATATCCAG TCCCTTCTAC  
12351 ATCATCCATG CCAGGGTGAT GAAAGAAGAT AGCAACAAC TCCCCCTTC  
12401 CCCCCAAGAG ATGCAAGCCC CACCCACAGA GACCAGTCCT GCTTATTGGT  
12451 GCCTGCTCCA CCCACCTCAC ATCTGCCCCG ACACACACAC ACCTTAGCCC

**Exon R2**

12501 CACTACTCAC CTCCCTCTCC CTCCTCTACA GCTTGGTCCT ATGTTCAAGA  
12551 ACACCAGTGT TGGCCTTCTG TACTCTGGCT GCAGACTGAC CTTGCTCAGG  
12601 TGAGACTTTA GAAGAGCCAG CCTGGGTGCC CAAACTTGTT CCCACTCTAA  
12651 AAGACTTTGC ACTGCTTCCT TGCTGCACTT CCTAGGTATA TCTTCACCAC  
12701 AAGGGGAATT CAGGAGTCAT TGGCTTGAGA ACCAGTTGTT TCCTGATAGT  
12751 AACACCCCCA TGCCCCAACT CAACATGCAA AATCTTCATG GTTCATCATC  
12801 AGGATTGAGA CACTACCCTG ATTACCCATC TGAATTCCCT CCTTTCCTG  
12851 ACCCCTCCCT TTCATTTAGG TGTTAAATTC TGTCCCAGG ATTTCTCTCA  
12901 AGATAACCAT GCCTCATCCA CATACTGCA TCCGCCTTTC AAGCTCATCA  
12951 CTAGTCTGAA GCTCTGGGTT CTCCTGTTCC CATGCCATGA GAATGCAGGT  
13001 TTCACCTTGC ACTTTTATAA AAATTATTAT ATCCATGACT CTGCTTGCAG  
13051 TCCCAGACCA AGATAGTGGT CTATGTACTC AGATAATCTA AGTGCAGATT  
13101 CTCACCTCTT TCCCAGATTT CTCATTTCCCT CTGGTTCCTT GATATGTTTC  
13151 CCTCAGCAAT CTCAAGACAA GTCCTAGGCA ATCTTTTCAT TGTCATTCCC

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**

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**Exon R3**

13201 CCTCCTACCT TCCTCAGGTC CGAGAAGGAT GGAGCAGCCA CTGGAGTGGA

13251 TGCCATCTGC ACCCACCCTC TTGACCCCAA AAGCCCTGGA GTGGACAGGG

13301 AGCAGCTATA CTGGGAGCTG AGCCAGCTGA CCAATGGCAT CAAAGAGCTG

13351 GGCCCCTACA CCCTGGACAG GAACAGTCTC TATGTCAATG GTGAGCAGCT

13401 GTGATATGGT AGGGGTCTCT TCCTCCTGGC TGTGCAACCA TCTAATCTCT

13451 GGCTTGGGGG CACACTCCCT GCCTGGCCAT TGAAAATTCT GTCACGTGCT

13501 CTACATGGGA TGACTAAGTT CTGGACTTCA TGGTTTCTTT GTTATCATGA

13551 GAGGCATTCC CTCTGGGCAC TCTTCCCTGT TGTGAGGATG CTGATAGGAA

13601 ATCTTTAATG ACCCCTGTCC CATGAAACTC ATTTAATTGC ACCAGGGTAG

13651 TCCTGAACTC TATCGCGTCC CCCACATCTC CTTAACCCTT ACCCAGTCTC

**Exon R4**

13701 CTCCCTCCTT CTCTATGCAG GTTTCACCCA TTGGATCCCT GTGCCCACCA

13751 GCAGCAGTGA GTATTCAACT CATGTCCATG ATGCCCCTGA TCCTACATCA

13801 AGTGGAGCAA GAGCTGGCCC CTCCTCTTTA ACCCATAAGT CCTCCTCTTG

13851 AGCAAATGAG CTGGGAAGGC AGAAGTTACT CAAGCTCCCC TCTGCCCCAG

13901 CTCCAAAGAC AGACCCAGCT CAAGCCCACA TGCAGCAGAC CTCATAATAG

13951 TCTATCTTCT TGCCATTTCT GCCATGAGAG TGCTTTCTGC TTCACTGAT

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**

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**Exon R5**

14001 GAGGACTTTT TTCAGCTCCT GGGACCTCCA CAGTGGACCT TGGGTCAGGG  
14051 ACTCCATCCT CCCTCCCCAG CCCACAAGT AAGTACCAGC CAATGGTATC  
14101 TGTATTAGAT CATGCCTGAT GAATGCAAAC ATCTGTGCCA TTTTCAGTCA  
14151 AATGAAAATG GAAAATCATA ATAAATCTAG TGATACTGAG TGAACCAAAA  
14201 AAAATGTATT GGCCACCTAC AGTGTACCAG ACCCTAGGGA TATAGCAAGG  
14251 AAAATAGAAC CAATAAAAAC ATCTCTGCCC TCAGTGAGCT TGTGTTTCATG  
14301 TGATGATATG ATGGTGGTGG TGGTGGTAAT AGTAATAATG ACATATTCAG  
14351 TTTGATGATA ATTTATGATT ATGGTGTTCG TGTGATGAT GGTGGTGGTG  
14401 ATGTTACTGA CAATGATGGT GACGGATCTT TGAGGATATT GTCCGTGATG  
14451 GTCGTGAAGA TTATGATGAT AATGATGATG TGTAAAGTGT GATGATGATG  
14501 ATGATCTGTG GTGATGCTGT TTAGGATGCT GTTCCGTGGT ACCGATGATA  
14551 TTGATGTTGG TCGTGGTTAT GTTGTATGAC AATGACAATG ATGGTGATGA  
14601 GGATAATCGC CAGTGATGGT GTGGGTTTAT GATGATGATG ATGTGTTGAA  
14651 TGTGGTGATG ATAATGTTCG TGGTGGTCGT GATGGGCATT ACTATGGCAG  
14701 TGATGGTCAT AATAATGATG GTGATGGTGA CAATGATAGC AAGGATGATG  
14751 ATGGCAATAA AGATAGTACA TAACATCAGA CAATATTGAG CTCTGAATAT  
14801 GCACCACGAG GAGTGCTCAG CATCTAAATA CTATTATATA ATATATTTTT  
14851 GTAAAAATAA ATTGTATTGT TTTAGGCAAG GGAAGCATGG TAAATATTTT  
14901 GTCACTCAAT TTAAATTCTG CATATGTTTA AAGATAAGTC TATTGCAAAC  
14951 TCCTATTTTC TCTACTTTGG ACATAGTGTT TGTTTCCCAC CTCCACTACA

Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**


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**Exon R1**

15001 GCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA  
 15051 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA  
 15101 CCACGGAGCG GGTCTGTCAG GGTCTGGTTA GTGCTCCACC CTCCTCACTC  
 15151 CGCCCCACCC CAGAGAGTCA GTACCTCCTA CATCATCCAT GCCAGGTGAT  
 15201 GGAACAAGAT CATACCCACC TCACCCTTGC CCCAAGAGAT GCAAGCCATG  
 15251 CCCATTGAAA CCAGCCCCAC TCACTGATGC CTGTTACTGC CCCACCTGAC  
 15301 TTCTGCCCTA CACACCCACA CACGCAACTT AGCCCTCCTA CTCATCTCCT

**Exon R2**

15351 TCTCCCTCCT CCACAGCTTG GTCCCATGTT CAAGAACACC AGTGTCGGCC  
 15401 TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTGAGA CCTTAGAAGA  
 15451 TCAAGCTTGG CTGCCCCACT TGTNNNNNNN NNNNNNNNNN NNNNNNNNNN  
 15501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
 15551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

**Exon R1**

15601 NGTGTTAGTC TACTTTTGAA CACTGTTTAT TTCCCATCTT CACTATAGCC  
 15651 GCCAGCCCTC TCCTGGTGCT ATTCACAATT AACTTCACCA TCACTAACCT  
 15701 GCGGTATGAG GAGAACATGC ATCAGCCTGG CTCTAGAAAG TTTAACACCA  
 15751 CGGAGAGAGT CCTTCAGGGT CTGGTAAGAG CCCCACATAC CTCATTCTAC  
 15801 CGCCACTCAC CATGTTTAGT CCTGCCACC TCACCTATTG CAGAGCATGG  
 15851 AAGATCTCAT CTACCTCATC TTGCCCCCAG ATATGCATAC CCCAACCCT  
 15901 GATGCCAGCC CCACCAACTG TTGCCAGCCC TGCCACCTC CTTTCTACCA  
 15951 CACCCTATG ACTTCAGTCC TCCCACTCAC CTCCCTCTCC CTCCTCCACA



Table 2 (continued)

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**Genomic Repeats**  
**(SEQ ID NO: 2)**

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**Exon R2**

16001 GCTCAGGCCT GTGTTCAAGA ACACCAGTGT TGGCCCTCTG TACTCTGGCT  
 16051 GCAGACTGAC CTTGCTCAGG TGAGAACTGA GAACAGCCAG TCTGACTGAT  
 16101 CTGAGCAGTT TGACCTGCTT CCCTTCTGCA CTCCCTGGAG ATGTCCGCAG  
 16151 CCAGGTGGAA TCCAGGAGGC AGTGGCTCTA AGACCAATGT GCTTCCTGTT  
 16201 CCCACCACCT CCCACCTCAA CTGAGAGATG CAGAGCCCAT CAGCAGGACT  
 16251 GAGCTTCTAC CTTGGTCATC CCTCTGAATT CCCTCCTTTC CCCTACCTGC  
 16301 CTTTCCACAA GTGGTTCAAT TCTGTTCCCA GGATTTCTCC CAAGAAAAAC  
 16351 ATGCCTCGTC CACTTGCTTT CATCCCCAAA CCTAGCTCTT CACCTGTCTC  
 16401 AAGTATGAGT TCTCCTTACC CCATGCTACA AGAATGCAGT TTCCACTTTG  
 16451 CAATTTTATA AAAATCCTTG CATCCATGAT TCTGCTCATA GTTGCTAAGA  
 16501 GTCAGTGCAC TCAGAGAATG GAAGTATGGC TTCTCACTTC TCTACCAGGC  
 16551 TTCTCATTTT CTCTGGCCCC CTCCTGTCCT GCCCTGTGGG ATCTCAGAAC  
 16601 CCCTCCCTAG GCAATCCGTG TATTGTCTTT CC CAATCTT GCCCTCCCCA

**Exon R3**

16651 GGCCCAAGAA GGATGGGGCA GCCACCAAAG TGGATGCCAT CTGCACTTAC  
 16701 CGCCCTGATC CCAAAGCCC TGGACTGGAC AGAGAGCAGC TATACTGGGA  
 16751 GCTGAGCCAG CTGACCCACA GCATCACTGA GCTGGGCCCC TACACACTGG  
 16801 ACAGGGACAG TCTCTATGTC AATGGTGAGT AGTTGTGATG TGGTTGGAGT  
 16851 CTCTTCCTCC TTGCTGGGCA GCCTCTACTC TCTGCCTTGA GGTCACGCTC  
 16901 CCTGCCTGGC TATTGAATGC TCATCCATGT TGTCTGTATG TGATGGCTGA

Table 2 (continued)

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**Genomic Repeats  
(SEQ ID NO: 2)**

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16951 GGTGGAAC TCAATGGTTTC TATTTTCATCT TGGACTGAGT TCATCCTCAG  
 17001 GATCTGCTTT CTGGATCTGA GGGTGCTGAT AGAGAATCTT CAATGGTTCG  
 17051 TGTTCCTGGA AATTCCTTCC ATTGCACCAG GGTACCCTGA CCCCTATATA  
 17101 GTTCCCCACC ACTCCCTTAA CCCTTACCCA CCCTCTTCCC TCCCTCTCTA

**Exon R4**

17151 TGCAGGTTTC ACACAGCGGA GCTCTGTGCC CACCACTAGC AGTGAGTATC  
 17201 CACTGATTTT CAGTGCTCCT GATCCTACAT CATGCAGGGC AAGAACTGAC  
 17251 CCCTCCTCAC ATGCCCCCTAT GTCTCTATG AGCAAAGGAG CTGGGACAGC  
 17301 ACAAGTTACT CCCTTTCCCT TCTGGCCCAA GTCTCTTCAG AGAGAGACCC  
 17351 AGCTCAAGCC CCACATGCAG CAAGGTCCAT AAATACTCCT ACCTGCTGGC  
 17401 ATTTCTGCCA TGAGAGGGTT CAACACTTTC ACTAATGAGG CCTTCTCCTC

**Exon R5**

17451 AGTTCCTGGG ACCCCCACAG TGGACCTGGG AACATCTGGG ACTCCAGTTT  
 17501 CTAAACCTGG TCCCTCGGGT AAGTACAAAT CAATCGCATC TCTGTTAGAG  
 17551 CATGCCTGAT GACTGTCAAC ATCTCTGCCA TTTTCACTTA AATAAAGATA  
 17601 AAAAATCCTA GTGAATCTAC GGATGAGGAG TCATCCAGCA AACTTAATTG  
 17651 AGTGCCTAGT TTCTGCAGGG CTCTAGGGAT AAGAAAGGGG ACACAAAACA  
 17701 GTTAAAAATA TCTGCTGCAA GAAAGCTTAT TTTATTGTGA GGGTGATGGG  
 17751 AGTTGGTGGT GGTGAAGTTA CTGGAGATGA TGACAATAAG AATGGTGATG  
 17801 CTAGTGATGA TGATGGTGAT AAGGATGATA ATTATGAAGA TGGTGGTGGT  
 17851 GATGATGATG ATGGTNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
 17901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
 17951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
 18001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Table 2 (continued)

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**Genomic Repeats  
(SEQ ID NO: 2)**

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18051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

**Exon R1**

18501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NGCTGCCAGC CCTCTCCTGG

18551 TGCTATTCAC TCTCAACTTC ACCATCACCA ACCTGCGGTA TGAGGAGAAC

18601 ATGCAGCACC CTGGCTCCAG GAAGTTCAAC ACCACGGAGA GGGTCCTTCA

18651 GGGCCTGNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

**Exon R2**

18851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNCTC AGGTCCCTGT

18901 TCAAGAGCAC CAGTGTGGC CCTCTGTACT CTGGCTGCAG ACTGACTTTG

18951 CTCAGGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNAGAAT

19001 TCAGTCGACC TACCGGCTTT GATGATTGCT CAGTTGAACT TAGAAATGCA

19051 CTGTCTGCCC AATGGTCCAG TCTCATGAGT GTGACTCTTT TCTGCCTCTC

19101 TTGGGTATCT GATCAAGATG GACTCAGGAA AAGTGCTCCA GATAACTGTC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
19151	TCCAATATAA	CACTGCCCCCT	GCCATCACAC	CCAAATGACT	GGAAGTTTCA
19201	CAGGGTCATC	AGCAGGGATT	GGACTTCCAC	CCCGGCCATC	CCTCTGAATT
19251	TTCCCTCTTT	TCTCCCCACC	TCCCTTGCCC	TTAGGTGTTA	AAATTCTCTA
19301	ACTAAGATTT	CTCTCAAGAC	AAATGTGCCT	CATTCACTTG	TTTAATTCCC
19351	AATTCAGCT	TGTCACCTGT	CTCAAGTCTA	GGCTGTCCTG	TCCCCATGCC
19401	ATGAGAATGC	AAGAACCACA	CTGAAATGTT	AGAAAAATTC	TTTTATCCAC
19451	AAGTATGCTC	ACCGTCCCAA	GCTGGACAGT	AGTCAGTGCA	CTCAGAGAAT
19501	CTAAGTGTGG	CTTCTCATCT	GTGTACCAGG	CTTCTCATTT	CCTGTGGGCC
19551	CTTCTTGTC	TTCCCTCCGC	AATCTTGGA	CTCCTCCCTA	GACAAAACCT
<b>Exon R3</b>					
19601	TATTATTATT	CCCCTCACCT	GCCCTCTCCA	<u>GGCCTGAAAA</u>	<u>GGATGGGACA</u>
19651	<u>GCCACTGGAG</u>	<u>TGGATGCCAT</u>	<u>CTGCACCCAC</u>	<u>CACCCTGACC</u>	<u>CCAAAAGCCC</u>
19701	<u>TAGGCTGGAC</u>	<u>AGAGAGCAGC</u>	<u>TGTATTGGGA</u>	<u>GCTGAGCCAG</u>	<u>CTGACCCACA</u>
19751	<u>ATATCACTGA</u>	<u>GCTGGGCCCC</u>	<u>TATGCCCTGG</u>	<u>ACAACGACAG</u>	<u>CCTCTTTGTC</u>
19801	<u>AATGGTGAGC</u>	<u>AATTGTGATG</u>	<u>TGGTTGGAGT</u>	<u>TTCTTCTTCC</u>	<u>TTGCTGAGCA</u>
19851	GGCCTCTACT	CTCTGTCTTG	AGGTCACCT	CCCTGCCTGG	CCACTGGTCT
19901	TGGCCATGTT	GTCTGTATTT	GATGATTGAT	ATGAACTTCA	CCGTTTCTTC
19951	TTCATCTTGT	ACTGGAGACC	TTCATCCTCA	GGACCTTCTT	CCCTGATCTG
20001	AGTGTACTTG	TATAGAATCC	TCAAAGCCCA	TGTTCCCTGA	AACTCCTTCA
20051	ATTGCACCAT	GGTAGCACTG	ACCCCTTTTG	GTCCCCCACC	TTNNNNNNNN

Table 2 (continued)

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**Genomic Repeats**  
(SEQ ID NO: 2)

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**Exon R4**

20101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTCACTCATC

20151 GGAGCTCTGT GTCCACCACC AGCACTNNNN NNNNNNNNNN NNNNNNNNNN

20201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

20251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

20301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

**Exon R5**

20351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNCCTG GGACCCCCAC

20401 AGTGTATCTG GGAGCATCTA AGACTCCAGC CTCGATATTT GGCCCTTCAN

20451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNGACTCCA GCCTCGATAT

20501 TTGGCCCTTC AGGTAAGTAC CAGTCAATGG CACCTCTATT AGAGTATGCA

20551 TGATGAGTGT CAACATCTCT GTCCTTTTCA CTCAAATAAG ATTAAAAATC

20601 ATAGCAAATT GTACGTGATG ATGAGTCACC CAACAACTT CTTTGAGTAC

20651 CCACTCTCTG CCAGGCCCTA GAGATAAGGC AGGGAACACA AAAGAGGTAA

20701 AAATCTCTGC CCTCAGAGAG CTTCTTTTAT TTTGAGGATG ATGTGGGATA

20751 GTGGTGATGA TGATGTTGCT GGAGATGATT ACAATAATGA TGGTGATGCT

20801 TATGACCATG ATGTGATGAT GATGGTGATT ATGAAGATGA TGATGATGAT

20851 ATTGATGATG GTAGTGGTTT TGACAGTAAT GATGATGTGA TGATGATGAT

20901 GATAGTGGTG GTGGTGATTA TGGGAAGGAT GACAGTGGTG GTGGTGATGG

20951 TGGTGGTTGT GGTGGTGATT GACAATGTGG TGGTGATATT GACAATGAGG

21001 ATGATGATGA TAGTGGTGGT GGTATGATG GTTAAGGATG ATGTGATGAT

Table 2 (continued)

		Genomic Repeats (SEQ ID NO: 2)					
21051	GGTGTGGTG	ATCACGGTAC	TAGTGGTGGT	GATGTGGACC	GTCATGGTTG		
21101	TGGTTGTGGT	GGTGATGGTG	GTGATCATGA	TGATAATGAG	GATGATGGTG		
21151	GTGATTGTCA	TGATGGTAAG	GATGAAACAG	TGATGGTGTT	GGTGACCATG		
21201	TTCCTGGTGG	TGATGGTGCA	GGTGATGATG	TGGATGATGA	TGGTGATGGT		
21251	GGTGGAGATG	ATAGGGATTA	TGAATATGGT	TCGGGTCTCT	GA CTGGTGGT		
21301	GGTGATGACA	ATAATGAAAA	TGATGGTCAC	AGTGTGGTG	ATGATGATGG		
21351	TGGTGATAAC	AAAGGTAATA	GATAGTGTCT	AGTATTATGG	AACACAGAAC		
21401	ATCACCAAAG	GTTATGCTCA	GCATCTAACT	ATTATTATTT	AGCATGCTCT		
21451	ATGAAAAACT	TTGATCGTTA	TAGTCAAGGG	AGGCATGAAA	ACCTTCTATT		
21501	TTATCACTCT	CTTTAAATCT	GGTTGCATAT	GTTTAGAAAT	AAATCTATTA		
21551	CAAACCTCTTA	AATGTTCTCT	ACTTTTGAAC	ATAGTGTTTA	TTTCCACCT		
<b>Exon R1</b>							
21601	CCACTACAGC	TGCCAGCCAT	CTCCTGATAC	TATTCACCCT	CAACTTCACC		
21651	ATCACTAACC	TGCGGTATGA	GGAGAACATG	TGGCCTGGCT	CCAGGAAGTT		
21701	CAACACTACA	GAGAGGGTCC	TTCAGGGCCT	GGTGAGAGCC	CTGCCCACCT		
21751	CACTCTGCCC	TGCCCACCTT	GTCTTGTTCC	ACCTACGTCA	CCCATTCCAA		
21801	GGCATGGAAG	AAGATCTCAC	CCACCTCCCC	TCACCTGAGA	GATAGCCCCG		
21851	CCCCCTGATT	ACAGCCCCTT	CCACCTTACA	TCTTCCTCAC	TTCTATGTCC		

Table 2 (continued)

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Genomic Repeats  
(SEQ ID NO: 2)

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**Exon R2**

21901 TCAGCCATCT TACTCACCTC CCTCTTCCTC CTCCACAGGC TAAGGCCCTT

21951 GTTCAAGAAC ACCAGTGTG GCCCTCTGTA CTCTGGCTGC AGGCTGACCT

22001 TGCTCAGGTG AGAACTGAGA ATAACCAGTC TGGCTACCCC AAGTGTTCCT

22051 AGGCCCCAAGG AGTTTCATCA GCTTTCTTCC TTCCCTCCCT ATGGAAGTCC

22101 TCAGCACAAG TGAATTTCAG GCGTTGGTGG CTCCAGGATG AACATATCTG

22151 CTGATCCTAC CACCTCCCCC ATCAATCGAG AGAATTTGCA GGGCCCATCA

22201 GCCAGATCAG GCTTCTACTT TGGTCATCCT TCTGAATTTC TTACTTCTCC

22251 CTACCTCCCT CTCCTTCAGG TGTAAATTC TCTTCCAAGG TTTCTCTCAA

22301 GATAAACATC CCCCATCCAC TTGCTTTCAT CCCCATTCC AGCTCTTAAT

22351 ATTTCTCAAG TCTGGGCTCT CCTGTCCCCA TACCATGAGA ATGCAATTTT

22401 ATAAAATTCT TGTATTCTG ACTCTACTCA CATTCCCAGG CTGCCTGGAA

22451 GTTGGTGCAT TCAGAGAATC TTAGTATGGC TTCTCACCTG TCTACCAGGA

22501 TTCTCATTTT CTCTGTCCCC TTCCTGTCCT GCCCCCAGGA ATCTCAGGAT

22551 GCCTCCCCAT AGGCAATCTA TTTAATGTCA TCCCCCTTAT CTGCCCTCCC

**Exon R3**

22601 TAGGCCAGAG AAAGATGGGG AAGCCACCGG AGTGGATGCC ATCTGCACCC

22651 ACCGCCCTGA CCCCACAGGC CCTGGGCTGG ACAGAGAGCA GCTGTATTTG

22701 GAGCTGAGCC AGCTGACCCA CAGCATCACT GAGCTGGGCC CCTACACACT

22751 GGACAGGGAC AGTCTCTATG TCAATGGTGA GCGGCTGTGA TGTGGTTGGA

22801 GATTCTTCCT CTTTGCTGGA CAGCTTCTTA CTCTCTGACT TGAGGTCACA

22851 CTCCCTGACT GGCCATTGAC GTCTTGGCTA TGTGTCTGT ATGTGATGAC

22901 TGATGTCTGA ACTTCATAGT TTCTTCATCT TGGACTGAGT TCATCCTCAG

22951 TACCTTCTTC CCTGATCTGA GGGTACTGAT AGAGAATCTT CAAAGGCCCC

Table 2 (continued)

		Genomic Repeats (SEQ ID NO: 2)				
23001	TGTTCCCTTGA	AACTTCTTCC	ATTCCACTAG	GGTATCTGTG	ACCCCTATTT	
23051	GATTCCCCAC	CTCTCCCTTA	ACCCTTACCC	ACTCTCCTCC	CTCCTTCTCT	
<b>Exon R4</b>						
23101	GTGCAGGTTT	CACCCATCGG	AGCTCTGTAC	CCACCACCAG	CAGTGAGTAT	
23151	TCAACCGATG	CTCCAGTAGC	CCCAATTATA	CACCAAGCAG	GGCAGGAGCT	
23201	GTCCTGTCTT	CCTATGCCCC	TATGTCCTCT	TCATAAAGGA	AGGGGCTGGG	
23251	AGGGCACAAAG	TTATTCCCTT	TCCCTTCTGG	CCAGCTCCAG	AGAGAGACCC	
23301	AGCTCAGGCC	CGATATGCAG	CAAGGCCTGT	AAATAGTTTT	ATTTGCTGAC	
23351	CTTTCTGCCA	TGAGAGGCTT	GGATGCTTCC	CCTGAAGAGG	GTTTCTCTGT	
23401	AGCTCTTGGG	ACTACCACAG	TGGACCTGGG	AAACTCTGGG	GATCCACCCC	
23451	TTCTACTGGT	CCCTTGAATA	AGTACCAGCC	AATGGCACCT	CTGTTAGAGC	
23501	ATGGCTGATG	AGTGTAACA	TCTCTTCCAT	TATTCAGTCA	AATAAAGATG	
23551	GAAATTCTTT	ATAAATCTAG	TGATGATGAG	CCAACCAACA	AACTTTATTG	
23601	AGCATTGTGA	CAAGCCCTGG	GGCTCTGCCA	AATCCTGGGG	ATATGGCATG	
23651	GATCATGAAA	CAATTAATAA	TCTCTCCTCT	CAGAGAGCTA	TTTTTATGAT	
23701	GATACTGATG	GTGGCAATGA	TGATGATGTT	GATGGTGATT	ATGACCATGA	
23751	TGACAATGGT	GATGGTGGTG	GTGATGATGG	TAATGATGAT	GATGGTGATG	
23801	TTGGTAATGA	TGGTGGTGAT	TATGACAATA	ATGATGGTGA	TGGTGACAGG	
23851	GATGGTGATG	ATTATGATGG	TGGTGGTGAT	AACAAAGTTA	ATGGATAATA	
23901	TATGAACTTA	TTGGCTACTG	AATATGCACC	AAAGTGCTAT	GCTCAGTGTT	
23951	TAACTAGTAC	TATTTAATAT	GATTTCATAA	AAAAATCTTG	AATTATTATA	
24001	GGCAGAAGAA	TCATGGGAAC	CTTTTATTTT	GTCACCTACT	TTAAGTCCTA	
24051	TTGCATATTT	TTTAAGTCAA	TTGCAAACAC	AGTTTCTCTG	CTTTGAACAT	



Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
24101	TGTGTTTATA	TCCAGTCACC	CCAATAGTGC	ATAAACCTGC	TGATTGGAGC
24151	AACTGTGTCT	TACTCCCTTG	TGCTTCCCTA	GTATCTGCTT	CAGGACCTTG
24201	TACATGGTAG	ATCGACAGAT	TTAGATCTAC	AGGAAAATAT	GGATTTTCCC
24251	AGGGAAGGAA	GGAATGAAGT	ATGCTTTCTT	ATAATGTATG	GAAACTTTCC
24301	TCTTCTGCCT	TGGTTCAACT	TTAGTGTCTG	CCAGAGTTTA	CACTGGAAAA
24351	CTATATGGCA	TCTGCTCCAC	TCCCTCATCC	ATGACAGACA	TCATTAATTG
24401	ATTGCAGCAT	TCATGGCAGA	CATCACCAAT	TGATAATAGC	ATTCATTTTC
24451	TCTCAGTTCA	AAACAGCTTC	AGAATGGTTA	CCAAAAAAAA	AAAATTCAGT
24501	CGCTACCAAT	TCAATTGGAG	CTGACTCAGG	ATTATGGGAC	AGAATTCAAG
24551	AGAGTTAGGT	TCCTTGATGA	TGTGTAGTGG	CTATTGTGTT	TCCGGTCCAG
24601	GCTAATNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
24651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
24701	CTTTGTGCGG	CAAAGTTCAG	GGGCCCCAAA	AATTTCTGTG	CCCAATCAT
24751	GGCGGACCTA	GGTTTAGGCA	CAAATTCAG	GCATTAAGTC	CCTGGAGATG
24801	TTATGGCTTT	TGGTTTTCTT	AGAAAGGCTC	AGCTCAGGCT	CAGCTTGGTC
24851	ATGCTGATAT	CCTTTCTTCC	ACTTGGTCGA	TTTGGCTGTT	GATACTTATG
24901	TATGCTTCAC	GAAGTTTTTG	TGCTGTGTTT	TTCAGCTCCA	TCGGTTGGTT
24951	TATGTTCTTC	TCTAAACTGG	TTATTCTAGT	TAGCAATTCC	TTTAACCTTT
25001	CATCAAGGTG	CTTAGCTTTG	CATTGCATTA	GAACATGCTC	CTTTAGCTCA
25051	TCGTACTTTT	TTATTGCCCA	TCTTCTGAAG	CCTACTTCTG	TCAATTCATC
25101	CATCTGATCC	TCCATCCAGT	TCTGCACCCT	TAATGGAGAG	ATGTTGCGGT
25151	CATTTGGAGG	AAAAGAGGCA	CTCTGGCCTT	TTGGGTTTTT	AGCATTTTTT
25201	TGTTGATTAT	TTCCCATCTT	CAGGAGTTTT	AGTTTCAGGC	TTTGAGGCTG
25251	CTGATCCTTG	GATGGGGTTT	TTATGGGGGT	CTTTTGTTTG	TTGTTGTGA

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
25301	TGATGATGAT	GTTATTGTCA	CTTTCTGCTT	GTTTTTCTTT	CAATAGTCAG
25351	GTCCCTCTTC	TGTAGGGCTG	CTGCAGTTTG	CTAGGGGGTTC	ACTTCAGGCC
25401	CTATTCATCT	GATTCGCTCC	CATGTCTGGA	GGTGTCACTC	AAGGAGGCTT
25451	GGAGAGCAGC	GAACATAGGT	GCCTGCTTCT	TCTGGGACCT	CTGACCTCGA
25501	GGGACACCAA	CCTGATGCCA	GTAGGATCGC	TCCTGTGTAG	GGTGTCTGAC
25551	AACTATTGTT	GGAGGGTTTC	GCCCAGTTGA	CTGGCATGGA	GAGCAGGACC
25601	CATTTAATGA	AGCACTTTGT	CCCCTGGTGG	AGAGGGGGTT	CTTCACTGGG
25651	GGGAAACCAC	ATGTCTGGGC	TGCTTGGATT	CCTCAGAACT	ACCAGAGGAG
25701	AGGCTAAGTC	TGCTGGTCCA	CAGAGACTAC	AGCCATCCCT	CCCACTAGGG
25751	GCCCAAGCCC	AGGGAGTCCA	AATTCTGTCT	CTGAGCCTCT	GGCTGGAGTC
25801	TTTGGAGATC	CTGCAAGGAA	GCTCTGCCCA	CTGAGGAAGG	ATGGGTCAGG
25851	GTTAGCCCTG	AAGAGGCACT	CTGGCTGCAG	ACTGCCACAG	CCGGTGTGTT
25901	GGGCTGTGGG	GACAAGTCTT	GGGACCAAGC	CGTCCAGCCT	ACCCGGCTCT
25951	AGCAGGGGAA	AAGTACAGCC	TGGAGCTATT	GAAAGGGGTG	CCGCCCTTCC
26001	CCCGCCCAGG	GAGCTTAGCG	TGTTAGGCAG	TTGTGAGTCC	AGTGCTGGCT
26051	GTCGCCCCCTT	CCCCAAGGAA	CAAAAAGAC	TTAGCAGGCA	GCCGCAGCCA
26101	GTGCTGGTCG	CCCCTCCCCC	GGGGAGTTCC	GTAGGCTTAG	GCAGATTCCA
26151	GCTGTAAGAA	TCTGCGTGTT	CTGGGGTTGG	GACACTAGGT	CCCAGTGGCA
26201	TGGGTTTCGCG	AGTGAGATCT	TCCAATCTGT	GAGTTGCACA	GTTCCGTGGA
26251	AAAAGCACAG	TTTCCCCCTC	TTGGGTAGCC	CGCTCACTCA	CCACCTCCCT
26301	TGGCTGGAAG	GAGGGGGTTC	CCCTTCCCCG	TGTGTCTCTC	AGGTGGGCCA
26351	CCACACCACA	CTGCTCTTCC	TTCTCTCTGT	GGGTCCTGTC	CAGCCTTCTA

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
26401	GTCAATTTTG	ATGAGGGAAC	CTGGACATT	TGGTTGCCAG	GAAGGATCAC
26451	ACACTTATTA	CAGTTTTTTTT	CAATGTGAGC	CTCTGAGCGC	TGCTGCTTAT
26501	AGTCGACCAT	CTTGGCCCCC	AGAGTCACAC	ATCTGTTATT	TTTTGATGTT
26551	TTGATTGTGG	CAATTCCTGC	AGAAGTAAGG	TGGTATCACC	TTATGGTTTT
26601	GATTTCCCTG	GTCATTAGTG	ATGTTGAACA	TTTTTTTCAT	ATGTTCATT
26651	GCCATTTGTA	TATATTCTTT	CAACAACTGT	CTATTTATGT	CCTTAGCCCA
26701	CTTTTTGATG	GGATTGTTTT	TTTCTTGCCA	ATTTGTTTGA	GTTCGTTGTA
26751	GATTCTAGAT	ATTAGTCCTT	TGTTGGATAT	ATAGATTGTG	AAGATTTTCT
26801	CCCACTCTGT	GGGTTGTCTG	TTACTCTAC	TGACTGTGAA	GGAAAAGTCA
26851	ATTTCTTATA	CGAATTTGTC	TCACTCCTAC	TTCCAAATGA	GATCCTGGGG
26901	TTTTTTTTTT	CTGTTAATCC	TTCACAATAC	TTCTCCCACT	TTTTTGA
26951	CATTTGTTTA	TATTCTGTTG	TCTGCTTCTC	TTTTATAGGA	ATGTGACTTC
27001	TTATGGGCTT	TCTCTATTAT	ACCACATATG	GGTTTTTGTT	TTGTTTTGTT
27051	TTGTTTTGTT	TTGTTTTTGT	CCTCGGATCC	ATTCTCCAAC	CTCCTCCAGC
27101	CTTCCCGTGC	TCTGTGGGAT	AGACGTCTGA	CTCATGAAAA	CTACATTTCC
27151	CAGGCTCCCA	TGCTAACTAG	CTTCCTGTTA	GGTTCAGCCA	ATAGGAGGCA
27201	TTGGTGGGAC	AATGGTGGGC	GGGGCTATGG	AAGGGCCAGA	GTATTTCTGT
27251	ACCCCGCCCC	CCTGCTCCCC	TTCCAATGTT	CCTGGAGCGG	TGTAGGACCA
27301	ATACTGTATA	TATGGAAGGA	AGGCAAGGTG	GATAGATTGG	AAGGAAGAAG
27351	TGACAGATGG	AAAGAAGAAG	TGATAAATGG	CAAGCGAGGC	AAGGGAGCAG

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)	
27401	AGGATGGATG AGTGGATTGC AAGAAAGAAA AAAATGGATG AAATATAAAA
27451	GGAGCAGGAC AGATGGATAA GTAGATGGAA GTAAGAAAAG ACTGGTGTAA
27501	GAAAGGAACG ATTGATGATG GATGATGAAT GGATCAGTGG TGATTGGGTG
27551	AAGGGATGAA TGGATGGATG GACAGATGGA TGAACAGATG GGTGGGTGGA
27601	TAGATGGATG GATGGATAAA ATGGGTAGGT GGATGGATGG ATGGATGGAC
27651	AGATGGGTGG GTAGGTGGAT GGATGGATAG ATGGATGGAT AAGTGAATGG
27701	ATGGATGGAT GGATGGATGG ATAAATGGAT GGATGGGTGA AAGGAAGGAA
27751	AGAAGTGAGA GAAGGAAGAG GAAGGATAGA CAGATGTTAG AAGGTACAAA
27801	TGAAAGGAAG GAAGCCAGCA AGAAAGAAAG GATGCATTAA TAGAATGAAA
27851	GATGGAAGGG AAGAAGAAAAG GATGGAAAGA GAGAAGGAAG AATGAACAGA
27901	AGGAAGTTCA AGAGTGGTGA AAAGAAGAAA GGCAGGGAGA GAAGGAGAAG
27951	TAAACTTTTC TTCTAGAGAT TTGTCTTAAA CCTTAGCTTG GCTGGACACT
28001	GTGGTTCACG CCTGTAATCC CAGCACTTTG GGAGGCCGAG GCGGGTGGAT
28051	CATGAGGTCA GGAGATCAAG ACCATCCTGG CTAACACGGT GAAACCCTGT
28101	CTCTACTAAA AATACAAAAA AAATTTAGTC AGGTGTGGTG GTGCATGCCT
28151	GTGGTCCCAG CTA CTCAGGA GGCTGAGGCA GGAGAATGGC ATAAAACCTG
28201	GGAGGCAGAG CTTGCAGTGA GCCAAGATCA CACCACTGCA CTCTAGCCTG
28251	GGCGACAAAG TGAGACTCTG TCTCAAACAA AAACAAAACA AAAAAACAAA
28301	AACAAAAAAC AAAACCAAAC CAAAACAAAA AAAAAACCT TAACTCATAC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
28351	TTTCATAAAG	TTCCACACAC	AGGGAGTGAT	TAGAAAGCAT	TTGCTGATAT
28401	ATTTTATATA	ATAAACATGT	ACACCATATT	GACCTGTGTG	CCCAGCAGTG
28451	CTTACATGAT	TTACAATGAT	TAACTTGTTT	AAGCTTCATA	ACAACGGTTG
28501	AGGCAGGAAA	CATCATTGTG	AACCATTGTC	ATCTCATTTT	ACAGATGAGT
28551	AAACTGAAGT	GCTGAGAGGT	TGGTTATGGC	TGCAAAGATT	GTTGGCCATG
28601	TTAACCAATG	CATAGAAGAT	TAGCATACCT	GGTTGTGAGT	GCAGGAGAGA
28651	GAGAGAAATG	GGAGAAAGGC	AGAGAAGGAT	CGATGGGGAG	AGAGGAAGAG
28701	AGAGAGAGAG	AATAAATTTT	TTAAAAATGT	CTAGAGTCAT	GACTTCCGCA
28751	TCAGTGTGGT	AATATGCAGC	CTTTACCCTG	GGAAAGATCA	GAACCATTGG
28801	TACTTTTAC	AGAATCTTCC	CTTCCTGCAT	TTGGGTAGAA	GGACCCCATC
28851	TGGACATCCC	AAATCATTAA	GCACACCCTT	ACTGGCTGCT	GGAGTTGTCT
28901	CCATTAAAAG	TCACCGTTGG	GTTTATTAAG	AGGCGGACAC	AGGGTCCTTA
28951	GAACACACTG	CCCCCACCTG	TCCCACACCA	CCCCCACCC	ACCCATCATC

**Exon R1**

29001	CTCCCCAAGA	GCTTCATCTC	TCTCTCTCTT	CCCCCTGCCC	TAGCCGGGGT
29051	<u>GGTCAGCGAG</u>	GAGCCATTCA	CACTGAACTT	CACCATCAAC	AACCTGCGCT
29101	<u>ACATGGCGGA</u>	CATGGGCCAA	CCCGGCTCCC	TCAAGTTCAA	CATCACAGAC
29151	<u>AACGTCATGC</u>	AGCACCTGGT	GAGAGGCCTG	CCTCCCGCTG	CAGCCCTGCC
29201	ATGCCCATCC	TAGGGCTGTT	GCCTGCCTGC	CTCTGACCAA	CCCAAGCTCC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)	
<b>Exon R2</b>	
29251	CTTCTCCCTC TGCAGCTCAG TCCTTTGTTC CAGAGGAGCA GCCTGGGTGC
29301	ACGGTACACA GGCTGCAGGG TCATCGCACT AAGGTGAGAA ACTCCCCAC
29351	CCACAGCGCA CCACCAAGAA CTTAGAGTTC TGA CTGGGAG GTCCCTCTTG
29401	GGTTGGGGTG GGCTACATAT TTTTTTAAAT CTTTTTATCT TTCCTTTTTT
29451	TTTTTTTGAG ATGAAGTTTC GCTCTCGTTG CCCAGGCTAG AGTGCAATGG
29501	CACGATCTTG GCTCACTGCA ACCTCTGCCT CCCGGGTTC AAGTGATTATC
29551	CTGCCTCAGC CTCCCCAGTA GCTGGGATTA CAGGCAGGCA CCACCATGCC
29601	TGGCTAATTG TTTTGTATTT TTAGTAGAGA TGGGGTGTCT CCATGTTGAT
29651	CAGGCTGGTC TTGAACTCCT GACTTCAGGT GATCCACCCT CCTCAGCCTC
29701	CCAAAGTGCT GGGATTACAG GCGTGAGCCA CCATATCTGG CCCCATCTCT
29751	TTTTTTTAAA TGAATTTAAG GAGTGCAAAT GCAGTTTTTG TTACATGCAT
29801	ATATTCCATA GTGAAGTCTG CAGACAGTAG ACTTCCAGAC AGTAGCTTCT
29851	GGTGTATCAC CCGAATAGTG TACATTGTAC TTATTAAGTG AGGTTCCCCA
29901	CCCTTCTCCC ACTCTCCAC CTTTCTGAGT ATCCAGTGTC TATTATTCCA
29951	CACTCCAGGT CCATGCTCTC ACGTATAAGT GAGAACGTAT GGTATTCCAC
30001	CATGAGCTAA TGGACATGGA GTCCATTGGC TCCCACTTAT AAGTGAGAGC
30051	ATGCGGTATT TGA CTATTTC TGAGTTTCAC TTAAGATAAT GGACTCCCAT
30101	TCCATCCATG TTGCTGCAAA ATACATGATT TCACTCTTTT TATGGCTGAA
30151	TAGTATTTTCG TGGTATATAT ATATACCACA TTTTCTTTAT CCAGTCTTCT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
30201	ACTGATGGAC	ACTTAGGTTG	GGTCCATACC	TTTGCTGTTG	AAATAGTGCT
30251	GCAATAAACA	TACACGTGCA	GGTGTCTTTC	TTATATAAAT	GATTTCTTTT
30301	TTTCTTTCCT	TTTTTTTGAT	ATAACGAATT	TCTTTTATTT	GGGTAAATC
30351	CCCCAATAGT	GGGATTGNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
30401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
30451	TGACCTGTCC	GTATTGATAT	ATAAAATGCT	GCATTTAAAG	TGTACAACTT
30501	GATATTTTGG	TATACATTGT	TAAATCATGG	CCACATTTCA	GCTAATTAAT
30551	ATATCTATTA	TCTCTACATA	GTTATCATGT	TTGTACCCTT	TGACCAGCAT
30601	CACCCCATTT	GCTCCTCCTC	CCAGCCCCTG	GCAACCACCA	TCCTACTCTC
30651	TGCTTCTATG	AGTCTGACAA	TTTLAGATTG	CACCTATAAG	TTAGATTATG
30701	CGGTATTTGT	CTTCTGTGTC	CTGGCTTATT	TCACTTAGCC	TAATGTCCTC
30751	CAGCTCCATC	TATGTTATCC	CAAGTGGCAG	GATTTTCATC	TTTCTTATAT
30801	ATTTCAATTG	ATATGTGTAT	GCCACATTTT	CTTTACCCAT	TCATCCATTG
30851	AAGGTCATTT	AGCTTGTTTC	CATATCTTGG	CTATTTTGAA	TAGTGCTGCA
30901	ATGAACATAG	GAGTGCAGAT	ATCTCTTTAA	GATACTGGTT	TCATTTCTTT
30951	CTTTCTTCTC	TTTTTTTTTT	TTCTGAGACA	GAGTCTGACT	CTGTCGCTCA
31001	AGCTGGAGTA	CAGTGGTGCA	ATCTTGGCTC	ACTGCAAAC	CTGCCTCCTG
31051	AGTTCAAGCG	ATTCTCGTGC	CTCAACCTCC	CAGGGAGTTT	TGCTCTTGCT
31101	GCCCAGGCTG	AAGTGCAGTG	GTGCAATCTT	CACTCACCAC	AACCTGTGCC
31151	TCCCGGGTTC	AAGCGATTCT	CGTGCCTCAG	CCTCCCAGGT	AGCAAGGATT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
31201	ACAGGCGCCC	AACACCACAC	CAGGCTAAAT	TTTTTTGCAT	TTT TAGTAGA
31251	GACGGGGTTT	TGCCATGTTG	GCCAGGCTGG	TCTCAAATTC	CTGGCCTCAA
31301	GTGATCCACC	TGCCTCAGCC	TCCTGAAGTG	CTGGGATTTT	ACAGGCATGA
31351	ACCACCACAC	ATGGCCTCAT	TTCTTTTAGA	TATATATGGG	TTGAGCTATT
31401	CTCAGAGGGT	CCTTTTCTGC	ATCTATTTAA	GATCACATTT	TTTTTATATT
31451	GTGGCAAAA	TACATGTAAC	ATAAAATCTG	CCATTTTAAC	CATTTTAA
31501	TGTACAATTC	AGTGACATTG	ATTATATTCA	CAATGTCATA	CAGCCATCAC
31551	CACTATTTAT	TTCTAATACT	TTTCCATTGG	GTAGATCCCC	AACAGTGGGA
31601	TTGCTGGGTC	AAATGGTAGT	TCTGATTTTT	TTTTTTTGTT	TTTTGAGAAA
31651	TCTCCATACT	GTTTTTCATT	TGAGGTTGTA	CTAATTTACA	TTCCCACCAA
31701	CAGTGTATAA	GAGTTTCCTA	GGCCGGGCAT	GGTGGCTTAT	GCCTGTAATC
31751	CCAGCACTTT	GCGAGGCCCA	GGTGGGTGGA	TCATGAGGTC	AGGAGATCGA
31801	GACCACCCTG	GCTAACATGG	TGAAACCCCG	TCTCTACTAA	AAATGCAAAA
31851	AATTAGCCGG	GCGTGGTGGC	GGGTGCCTGT	AGTCCCAGCT	ACTGGAGAGG
31901	CTGAGGCAGG	AGAATGGCAT	GAACCCTGAA	GGCGGGGCTT	GCAGTGAGCT
31951	GAGATCGCAC	CACTGCACAC	TTCAACCTAG	GCGACAGAGC	GAGACTCCAT
32001	CTCAAAAAA	AAAAAAAAA	AAAAGGTTTC	CTTTCAGTGC	ATCCTTGCCA
32051	ACTTGAGTTT	TCTGGGTTGG	TTTGCACTCT	CATGGTATTT	ACTAGATACT
32101	TCTCCATTTA	TATTTTTACT	CAACCCATGC	CCATAACACC	ACTCCTCTAC



Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
32151	CATTCCCACC	AACCATGTAT	AAGAGTTCCT	TTTCTTGCAT	CCTTGCCAAC
32201	TTGACTTCTT	TGGGTCAGTT	TGCACTCTCT	TGGTATTTAC	TATTTACTTC
32251	TCCATTTATA	TTTTTAGTCA	ACTGATGCCC	ATGGCACCGC	TCCTCTGAGG
32301	CAGGTGCTGG	GTA TAGAGT	GATAAGACAG	ATGCTGTCCC	TGCCCTCACC
32351	CAGTGGAGAA	GAACAGATGC	TAAACAGGAA	CATAAATATC	TAAGTAAAAT
32401	GGCTTCAAAT	GGAGTAAAGT	GATATGAAAC	ATAAATAAAT	AGCAAGTGAT
32451	GGGTAGAGCA	ACTTTACCCA	GGATGAATCT	TGGGCTGTGT	CCCAAATGGC
32501	CATGAAAAC	GTTCCAGGCA	GGGAGAACAG	CATGAGAAAA	GGTCTTGAGG
32551	TGCAAATGAG	CTTGGCATGT	TCTATGAACA	GCAAAGAGGC	CAGTGTGGCT
32601	GGAGCAGAGA	GAGAGCAAGA	AGAAAAGAGA	GAAAGGATGA	GACTCAAGAC
32651	ATCAGCAAGT	TTGAAGGGCC	TTGGAGGACT	TGGATTTTTT	TTTTTAAGAC
32701	AGCTTTGTTC	TTGTTGCCCA	GGCATGATCT	CGGCTCACCA	CAACCTCCGC
32751	CTCCTGGGTT	CAAACGATTC	CTCTGCCTCA	GCCTCCCAG	TAGCTGGGGG
32801	TAACAGGCAT	GTGCCCACCA	CACCTGGCTA	ATTTTGTATT	TTTAGTAGAA
32851	ATGGGGCTTC	TCCATGGTTG	GTCAGGCTGG	TCTCGAACTC	CCGACCTCAG
32901	GTGATCCGAC	CGCCTCGGCC	TCCCAAAGTG	CTGGGATTAT	AGGTGTGAGC
32951	CACTGCACCT	GGCTTGGATT	TTTTTTGTTC	TATATTGTGG	TAACATACAC
33001	ATCACATTAA	ATTGATCATT	TTAGCTATAT	TTCCCGTTCA	GTGGCATCAA
33051	GCACATTCAC	ATTATTGTGC	AACCATCACC	ACTATCATCC	ATCTCCAGAA
33101	CTTTCTCATC	TTCCCAAAC	GAAACTCCAT	CCCCATGAAA	CACTCATTCC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)	
33151	TCATCCCCCT CCTCAAGCCT CTGGCACCCA CCATTCTACT TTCTGTCTCT
33201	GTGAATCTGA TGATTCTGAG GACCTCCTAT GAATGGAGGA ATCATATGGT
33251	ATATGTCCTG GTTTATACTG TATGGCTGGC TTATTTACC AAGCATAATG
33301	TCCTCAAAGT TCATCCATGT TGTAGCATGT GTCAGAATTC CCTTCCTTTT
33351	CCACTTGTAT GTAAATGCTG TATTGTGTTT CTCCATTCAT TAGGACTTTG
33401	ATTTTTGCAG GGAGTTGTCA AGGGGTGCTG GGTTCCTGGG CTTCAATATA
33451	ATAAGAGTAA GCTAAACTGG TTCATTTCTT CCTTCGTGGA GACCATGTTC
33501	TGGTAGGAAC AGGAACAAAT AATTTATGAT TACATAGAGG GTGACCAGGG
33551	CAGTGACAGG GGAAGAGTGG AGGATTGTGG GACCCAGAGG AGGCTCCTGA
33601	CCTTGCCTAG GAAGATAGGA GGAGGAAGAG GAGGAGGAAG AGGAGGAGGA
33651	AGAGGAGGAG GAGGAGGAGG AGGGAGTCCT CTAAGCTGAG ACCTGGAGGA
33701	TGACCAGGAA GTTATCCAGG TAAGGAGAAA TGGGGAGAAG CTTCCAGACA
33751	AAAGTAACAG CAATTGCAAA GATCCTGAGA TGATAGATAA GGTCAGGTGG
33801	AGAAAGTGCA AACTGTCAAT GAGACCAAAA TATGGACTGT GAGTTGTGCA
33851	GTGACCACAA GTGGAGAGGT GCTAGGTGGC CTTTCATCCCC CAAAGCTGCA

**Exon R3**

33901	<u>CCTCTCCCTC CTCAGGTCTG TGAAGAACGG TGCTGAGACA CGGGTGGACC</u>
33951	<u>TCCTCTGCAC CTACCTGCAG CCCCTCAGCG GCCCAGGTCT GCCTATCAAG</u>
34001	<u>CAGGTGTTCC ATGAGCTGAG CCAGCAGACC CATGGCATCA CCCGGCTGGG</u>

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
34051	<u>CCCCTACTCT</u>	<u>CTGGACAAAG</u>	<u>ACAGCCTCTA</u>	<u>CCTTAACGGT</u>	GAGCAGCTAT
34101	CAGCCCCATC	TCCCTGCCCC	ACCCCCCAGC	CCCCACTGCA	GTCCAGGAGG
34151	GTGTCTGTTT	GCCGGTTCTC	TAGGGAAAGA	CTTGGGGTTC	AAGTCTTGGC
34201	ATTACCACTG	GCCCTCCCAT	AACCACAATG	CAAGGTTGGA	CTTTGATTAA
34251	TCCCATTTTA	CAGATGAAGA	AACTGAGGCT	TAGACAGGCT	AAGCAATTTA
34301	CCTTGACAGT	GGTGGAACCA	GGATATGAAC	TCCACTTGTC	AGCATTCGGT
34351	GCTATGATCC	ACTCCACATG	TTTAACTCAC	AGAAGAGTCT	TCCTGGTGGG
34401	GGCACTTGGG	GGACAAAAAA	CACATTTCCG	GCTGTGAGCA	GTGGCTCACA
34451	CCTGTAATCC	CAGCACTTTG	GGAGGCCAAG	GCGGGCGGAT	CACAAGGTCA
34501	AGAGATTGAG	ACCACCCTGG	ACAACATAGT	GAAACCCTGT	CTCTACTAAA
34551	AATACAAAAA	TTAGCTGGGT	GTGGTGGCGC	ACGCCTGTAG	TCCCACCTAC
34601	TCGGGAGGCT	GAGGCAGGAG	AATCGCTTGA	ACTCGGGAGG	CAGAGGTTGC
34651	AGTGAGCCAA	GATTGCGCCA	TTGCACTCCA	GTCTGGGTGA	CAAGAGTGAA
34701	ACTCTGTCTC	AAAAAAAAAA	AAAACAATTT	CCCCTCCCTG	CTTCTTCTC
34751	ACCATTGACG	AGGGATGGGC	TTCTCTCCTA	CCTGAGGCCC	CCTATACCAG
34801	GAAGATCTAT	GGGATCTAAT	CTTCAGCGCA	CACTGGGCCT	CAGCATTGGT
34851	CTAGAACTCA	GGATAAGATA	GCATTTAAGA	AGGCATCCCC	TAAATGGGGT
34901	TCTGAGAGGC	AAAGCATGAC	CGTGGAGAAT	TGACAAAATA	GCTCGCCTTT
34951	CATCCCCTCC	ACCGCCAACC	CAAGAACAGT	GCTTATCATC	ATGACCCCAT
35001	GAGGTGGGCA	CCCCATATCA	CTTATATGAG	GTACCTTTAG	GTAGGTACCG

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
35051	GGATGTGGAG	AGACATCCTG	GGCTTTCATT	ACTCTTATTT	TAGCAAAGAG
35101	GGAATCTGAG	GCACAGAGAA	GGAAGGGAC	TTGCCCATGC	CCACAGCGAG
35151	TTTTTGGCTA	GTATGGGTCT	TGATGTTCTT	TCTGGGTCCG	TNNNNNNNNN
35201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35251	NNNNNNNNNT	TCCTGCGTGG	GAGATGTGTG	GATTTGATTT	GSTATCTGGAA
35301	AGATGATTTT	TTATTGGTGA	CAAAGCAGTT	AAAGTTAATC	TTCACAGTTG
35351	TGCGGAGAGT	GACCACGCGA	GTTAGTCTTA	TCCTTATTTT	TTTGATCATC
35401	CCGCTACACA	AGACAAAGCG	AACCGCACAG	GCAACATCAG	CAGGCCCCAT
35451	TGGTGTGTTT	CCCTCTATGG	GTCCATGTGT	TCTCATCATT	AGCTCCCACG
35501	TATAAAGTGA	GAAGATGGCA	GTATTGGTTT	TCTGTTCCCTG	CATTAGTTTG
35551	GTAAGGATAA	TGACCTCCAG	CTCCAACCAT	GTTCCCTGCA	CGGACATGAT
35601	CTCATTCTTT	TTTATAGCTG	CATAGTATTC	CATGGTGTAT	ATGTTCCCTCA
35651	TGTTCTTTAT	CCAGTCTATC	CTTGATGGGC	ATTTAAGTAG	ATTCCATGTC
35701	TTTGCTATTG	TGAATAGTGC	TTCAGTGAAC	AGGTGTCTTT	ATGATAGAAA
35751	AATTTATATG	CCTTTGGGCA	TATATGCAGT	GATGAGATTG	CTGGGTCAGA
35801	CGGTAGTTCT	GTTTTTAGCT	CTTTGAGGAA	TCATCCTGCT	GCTTTCTACA
35851	GTGGATGAAC	TAATTTACAC	TCCCACCAAC	AGTGTATAAA	CACTCCTTTT
35901	TATCTGCAAC	CTCAGCAGCA	TGGTTTTTATT	TCTCTTTATG	GCTGAATAGT
35951	GTTCCATTGT	GCATATATAC	CACACTTTCT	TTATGGATTG	ATCTGCTGAT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
36001	GGACATATAG	GTTGATTCCA	CATCTCTGCT	ATTGTGAATA	GTGCTGTGAT
36051	AAACACACAG	GTGCGGGTTG	GGTCTTGATG	ATCTCAGTTA	ACATCCAGTC
36101	CCTTCAACTT	GGCTATTGCA	GGGAGCTGTT	CCCCCTTGTA	AACTGCACAG
36151	CTTATGTGCT	TCATTTTGTT	CCTTCATTTA	GATTTACCAA	GCAGCTACTA
36201	TTAACCAGGC	CACAATGTGC	CTCGCCCCCA	GGAACAGAGA	TAGGTTACAT
36251	GTGCATCCTG	TCCTAATGTA	ATCTCCAGGG	GGGCGGAGAC	TGTTTTGTTC
36301	TACCCTATAT	TCCCCAAATG	TAAAGGGAGC	CTTGACACATA	CTAAGCCCTT
36351	AATAAACATT	CATTGGGTGG	AGGAATAGAT	TGGAGGAGGC	CTGGAAGGGG
36401	AGGCGGGGGT	TATGGATGGA	TAGGAGGATA	GACTTGTGAA	CACAAAGGTA
36451	GTGAGAGCCT	CTCATTGGAG	GCATGCTGGA	GACGTGAGTA	GGGAAGGGTC
36501	AGTGCTAATT	GAAATATCAG	GAAATTCTTT	CTAGTGGTGA	ACACATTTAA
36551	GTCAAATATT	AGATGATACA	TAAATGTATC	CATAATCTCT	AGATACACAA
36601	AGGGAAAGGC	ATCCAGGCAG	GGGCCCCATA	TGGACAAAGG	CATGGAGTAT
36651	CTGGGACGGT	TCCACCACCT	CCTCTTACGT	GTGACTTCTT	TGTTTCAAGG

**Exon R4**

36701	<u>TTACAATGAA</u>	<u>CCTGGTCTAG</u>	<u>ATGAGCCTCC</u>	<u>TACAAGTACG</u>	TGTCTTTGAA
36751	TCTAGTGCCC	ATTTCAATCT	CCATGGGTCT	TGGTTCAAGC	TTTCTCCTC
36801	ATTCATGAAG	GAAGGTTGCC	CCAAATTCGG	GCTGGTCCCC	TAGGTGGTGA
36851	GGGGCATTGT	CTCAGTGGGA	GGAAGAATGC	TGAGTCCTTG	GCCCTGTTTT
36901	TAGACCTGCA	GCCATAGTCT	TGGCTTTGTG	AATTTTCCAT	GTCCCTCTGG

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
36951	GTTGGAGGAA	GAAGTTTGAA	CAAGCATTCC	CTACACGGGA	TAGAGGTTGA
37001	GGTCAGATGA	TGACCTCTGT	TAGTCTGTAC	CCTCCTTGAT	AAGAAAATCT
37051	CCTCCAAGTG	CCCCAGCAGA	GGCTTCATGG	TCAAGCTGCA	GACTCTGCTG
37101	GCTACTGGTT	TTGGCTAAAT	TTGCCATTG	CCTCATCCAG	TGATCCACTC
37151	GTCTATCTTT	CCAGCCATCC	ATTTTCTAT	CCTTCCAGTC	ATCTCTCAGA
37201	CACCACCTGT	CCTTCCATCC	ATCCATCCGT	CCATCCATTT	ACCCATCCAT
37251	CCATCCACCC	CATTTTCCTG	ACCATTTACC	TCCTCGTCCT	TCCTTCCATC
37301	TGTCCTTTTA	TCCATCTATT	CATCCATCAC	CCATCCTCCT	GCCCATTCAC
37351	CTGCTTGTC	CTCCTTCTT	CTGTCCTTCT	ATACATCCAT	CCATCCATCC
37401	ATCCATCCAT	CCACCCATCC	ACTCATCCAC	CACCCACCCA	TCCTTCTGCC
37451	CACTCACTCG	CTAGCCCCTC	CTTCCTTCTG	TCCTTCCATC	CATCCATCCA
37501	CCCATCTTCC	TGCCCATTCA	CCTGCTTGTC	CTTCCTTCTA	TCTGTCTTTT
37551	ATCCATCTCT	CCATCCATTC	TCACCATCCA	TCCATCCATC	CTTCTCCCTA
37601	TTCACTGGTT	TGTCTTTCCT	TCTGTCCTTC	CAACCATCCA	CCCATCTCTC
37651	CATTCATTCT	CCTCTTCATT	CACCATGTTT	CCTTATTTCT	GTCTCTTCCA
37701	TCCATCCATC	TATCCAGACA	GACATCTCCT	CCCCCATTC	TCCTCCCCAT
37751	TCACTCAATT	GTCCTTCCTT	CCATCTGTCC	TTTTATCCAT	CCATCCACCC
37801	ATCCATCCAT	CCATCTATCC	TTCTCCCCAT	TCACCTGTTT	GTCCTTCTTT
37851	CTGTCCTTCC	AACCATCCAT	CCATCCATCA	TCCATCCATC	TATCCTTTTC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
37901	CCCATTACACC	TGTTTTGTCC	TTCTTCTGT	CCTTCCAACA	TCCCTCCATC
37951	TCTCCATCCA	TCCTCCTGCC	TATTCATCTG	CTTGTCTTTC	CTTCCTTCTG
38001	TCCTTCCATC	CATTCATCCA	TCTGCCCATC	CACCCACTCA	TCCTCTTGCC
38051	CATTACCTG	CTTGTCTTTC	CTTCCACCTG	TCCTTTTATC	CATCCATCCA
38101	TCCATCCATC	TTGCTCACTC	CTCCACTCAC	ACAATCACTC	CTTCCCTCAG
38151	TCTCATTTAT	GGCCACCTG	TGAATGGTTG	TCCTGGCTTG	GACCACTGAT
38201	GAAGCCCAGG	GGAGCTTCTC	CCACTAGTGG	TGGGCTTTTG	TCCTCTCTGA

## Exon R5

38251	TGGACTGTTC	CTTCCACAGC	<u>TCCAAGCCA</u>	GCCACCACAT	TCCTGCCTCC
38301	<u>TCTGTCAGAA</u>	GCCACAACAG	GTATTTGGGG	CCATTTTTC	TCCTCGAAGA
38351	TTAGAATAGC	ATTTCAATCA	GACACCTGCC	CTCGTGGAGT	CCCAGATTTT
38401	ATGAAATAAA	TAGACCATCA	TAATGTCAGA	TGTTTTGGGG	TGAGATACCT
38451	GGCATAGTTG	GGAAGGAGGA	GGGCTTTCTG	GAGAAAGTTT	CACCTGAACT
38501	GAGTCTTTAA	GGATGACTAA	GAGTGATTCA	GGCAAATAGG	GCATGAATAG
38551	TATAACTGAA	AGAGGGGAAT	CTGTGAGCAA	AGCCTCAGTG	GCCAGAAACA
38601	GCATAGAGTA	TAGGGAGAAG	TGAGAGAAAT	TTGGTTTGCA	TGAAACATAA
38651	AGCTTAACCC	AGAGTGGATG	GATAAGTGAG	ACTGAAAGGT	CAGCAGGAGC
38701	CAGATTGGGA	AGGGCCTTGA	ATGCCAAGTC	AAGAAATTTG	AACTTAACAC
38751	TGAAGGCCAT	AGGGAGCTGT	GGATGGTACT	AGAGCAGGGG	CAGCCATAGT
38801	GAGATTGTCA	TTTCAGAAAG	ATTCTTCTTG	TGTTCAGTAT	AGAGAATGTC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)	
38851	CTTTAGACAG GGCATCCAGT GAGTCTGCCA GGTGCTAATC AGGGTGAGAG
38901	AAAATAAGAC CTGAACTGGG ATAGGGGGAG GAGAGAGAGG ATATATGTGA
38951	TGAATATTCA GTAAAGAGAA TTGGTGTTAC TTGGAGGGGA GAAGACACAT
39001	AGCTTCTGAC TTGCGATGGC CACACTCAGT TTAATAATGA GCGCAGTCTG
39051	ATCTAGTCTC AGACCAGCCC TCAGTTGCAG ACGTCTCTCC TCCCCTCCTG
<b>Exon R1</b>	
39101	CAGCATGGGG <u>TACCACCTGA AGACCCTCAC ACTCAACTTC ACCATCTCCA</u>
39151	<u>ATCTCCAGTA TTCACCAGAT ATGGGCAAGG GCTCAGCTAC ATTCAACTCC</u>
39201	<u>ACCGAGGGGG TCCTTCAGCA CCTGGTGAGA CCCTGGTCCC AGCAGCTCCT</u>
39251	GGTGGGATAA ATCCTACCCC CAACCTCTGT TCCTCGGCTT ACCCTCTTCC
<b>Exon R2</b>	
39301	TCCTTCCTCT <u>CAAGCTCAGA CCCTTGTTCC AGAAGAGCAG CATGGGCCCC</u>
39351	<u>TTCTACTTGG GTTGCCAACT GATCTCCCTC AGGTGAGACC ACTTCCTGGC</u>
39401	CATTTGCCAG TAACAACCAC CCCTTTTGTG ACCACCCCTT CCTCAGCTTT
39451	CCCCTGCTCC TCCCTCCACT GCTCTTTACC TGCAGAGGTC TCGGGACCTC
<b>Exon R3</b>	
39501	TCTAGAGTCC TCAAATGCCT CTCTCCCCAG <u>GCCTGAGAAG GATGGGGCAG</u>
39551	<u>CCACTGGTGT GGACACCACC TGCACCTACC ACCCTGACCC TGTGGGCCCC</u>
39601	<u>GGGCTGGACA TACAGCAGCT TTAAGTGGGAG CTGAGTCAGC TGACCCATGG</u>
39651	<u>TGTCACCCAA CTGGGCTTCT ATGTCCTGGA CAGGGATAGC CTCTTCATCA</u>



Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
39701	<u>ATGGT</u> GAGTG	TCAGGCTGAA	CTTGGATTTA	CAGTGACTTT	TGGGGAGTTG
39751	GTTTCTTTGT	TTTTGAGATG	GAGTCTCACT	CTATCACCCA	GGCTGGAGTG
39801	CAATGGTGCA	ATCTTGGCTC	TGCAACAGTG	ATTCTCCTGC	CTCAGCCTCC
39851	CAAGTAGCTG	GGATTTACAG	GTGCATGCCA	CCACGCTCAG	CTAATTTTTG
39901	TATTTTTAGT	AGAGATGGGG	TTTACCATG	TTGCCCAGGC	TGGTCTCGAA
39951	CTCCTGACCT	CAGGTGATCC	ACCTGCCTTG	GCCTCCCAA	GTGCCAGGAT
40001	TACAGGCATG	AGCCACCATG	CCCGGCCAC	CATGACTATT	ATTTGTCCCT
40051	GTTGTATGCC	CTTTCCTCTC	TAAAAAAAT	AGCCCAAGGC	CTGGCTGGGG
40101	GACACCCTTC	CCCAAACCAC	CAAGGGGAGG	GTCTTCCCA	TTATTTTGAG
40151	TAAATAGCAT	GAAATTCTTT	GACCAAATTA	ATGTCATAAA	TTGTTTGTCT
40201	CTTCTCCTT	CACTTTTGTT	TCCAACCTGG	TTGCGGTATA	ACTATCAAAT
40251	ACAATTGTAT	GTATTTAAGA	TGTATAATGC	AGTGATTTAA	TATATGTGTA
40301	GCTTATGAAA	TGATTACCAT	GATCAAATTA	GTTAACACTG	CTTTCATGTC
40351	ACATAGTTAC	CGTGTGTCTG	TGTGCGTCTG	TTGAGTTAG	AGAGAAAGAG
40401	AACATTTAAG	GTCTACCCTC	ATAGAAAATT	TCAGGTTTAC	AATACAGTAT
40451	TATTAECTAT	AATCATCAAG	CTTTATACTC	GATCCCCAGA	ACTTATTCAT
40501	CTTGTAECTA	AAAGTTTGTA	TTTTGTGACC	AACATCTCCC	CATTTTCTCT
40551	ATCACCACCC	CCATGCCCCC	AGCCCCTGAT	AACCATCATG	CTACTCTCTG
40601	CTTCTGTAAG	TTTGACTTCT	GATCCACAT	ATAAGTGAGA	TCATGCAGTA
40651	TTTGTTTCTC	TCTATCTGGT	ATATTTCACT	TAGCATAATG	AACCCCCCCC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
40701	AGGTACATCC	ATAATGAATT	TCAATTCAAA	ACCCAAGTGG	CTGAGTCGTG
40751	GCATCCTTTG	GGACAGGATA	GCAGGTCCCT	TCTATATAAG	GATCCTCTGT
40801	GTCAGTGGTT	ATTACCAGGG	GACAATTCTG	CACTTCTGCC	CCACCCCACC
40851	CCCCAACTGG	GAGACTCTAG	GCAATATCCG	AAATCATTTT	TGGGTATCAC
40901	AACTCAGGGA	GGGAAGGAGG	GTGCAACTGG	CACCTAGTGG	GTCGGTAGCC
40951	CATTTTCCAG	TGCACAGGAG	ACAACCACCC	CAGGGAATGA	TCCAGCCCCA
41001	AATGCCAATA	ATTTCAGGG	TGAGAAATCC	TGTTGTACAT	GGTCTCAAAG
41051	TTCTTAGGTG	GGCACAAGGC	TGACATTTAT	CACACTTTAC	TGTAATTACT
41101	TGTTAAATTT	ATCTGATTCC	CCCTTACCCT	GTGAACTCAA	CAAAATTACG
41151	GTCTATTATG	AGTGCCACTG	TACCCTCGGT	TCGCAGTACA	TCAGCACATC
41201	ATAGTATGGA	AAGAATCATT	GAATGAGTGA	GCAAATTAAA	GATTTGTGTC
41251	TCTGCTGTAA	CTCACATTCA	TTAATTCATT	CATTCAGCAA	ACATATATGG
41301	GTGGCTGTTC	TGCCCCAAGC	CTTGTA CTGG	GTCTGGAGAT	AGAAGACACA
41351	TTTTTCTGTC	TCTGAAAAAC	TCATACTCAA	GTTAACAACA	AATTACGGGC
41401	ACAACAAAGA	CCCCACTGCT	GTTATTAACA	GGGTACTATG	GGAGCTGAGA
41451	GGAGGAGTAA	ATTAAGGAGG	GCTTCCTGGA	GGAGGGTGTT	ATATACCCGG
41501	CCCTGTGCCG	GGACACATAA	TGATAAGACA	GACTTGGGCC	TCTGCTGTCC
41551	TGGAGCTCCC	TCTCACTGGG	CTCTTGAAGC	GTGAGCAGGA	GTTTTGCAGG
41601	AAATGAAAAG	GATGCATTCC	TAGAAGTGGG	AACTGCATAG	CACATGCAGG

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
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41651 AAAGCTCAGC TCAGAAGAAT CTGTGTAATA TTCCATTTTT CCCTCTCTTT  
 41701 GGGGCAACTT TCTGTCTAAG AGCTCCTGCA ATGCCCAGCG TGTGGACCTG  
 41751 AAATTGATTC TGACAGTAGG CAGGGGACTG CTGGGCAACT TTGGCTCTGC  
 41801 ATTTTGTGAT CAACATTTCC CCACCATATG TTGCCTTTTC TTCTTCTCTG

**Exon R4**

41851 TGGCTCCAGG CTATGCACCC CAGAATTAT CAATCCGGGG CGAGTACCAG  
 41901 ATAAATTTCC ACATTGTCAA CTGGAACCTC AGTAATCCAG ACCCCACATC  
 41951 CTCAGAGTAC ATCACCTGTC TGAGGGACAT CCAGGACAAG GTGGGGCATC  
 42001 TCTCACCCCT CCCGTCTTCT CTGTCCTGTG TGCTTCTCTC CCTCTTCTAC  
 42051 CTGATTTCTC TGTTAAGTGA TCACTTTAAA TGCTTCACTT CACTATGTAT  
 42101 TCTGGGTTCT CTCTCAGTTT CAAAAGTAC TCTCTTGACT ACCATTCCCA  
 42151 TTTCACAGAT GGGCAAACCTG AGGCTCAGAA AGGGGCGTGG TGTGCCTAGG  
 42201 GTCATACAGT GCTTTAGGAA CAGAGTTAGG ATTTGAACTC TGGTCCCCTT  
 42251 TGCTCCAAGT CCTGTGTTTT TTTCCACTGG CATCAGCGGC CCCTCCACCC  
 42301 CCAAGAGGCC TCCATCTCAC CCACTCTCCC TACCCATCTT TCTAGGTC

Table 3

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**Genomic Carboxy Terminal**  
**(SEQ ID NO: 3)**

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**Exon C1**

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1  ACCCACTCT ACAAAGGCAG TCAACTACAT GACACATTCC GCTTCTGCCT
51  GGTCACCAAC TTGACGTAAG TTCTGAAGGT CATAAGCAGT GACCAAGCTT
101 GTGGCTGTGT CTCTGAGCAC CCTTGAGCTA GACGTCCCCA GTGGGGTACC
151 CATTCTCCCC TACATCCCTG TCTAGCTAAT CCTACCATCT CCTCCCATAA
201 ATCCTCAAGG TAGGGAGTGA GGATTAACCT CATGGGGCCA CCAACTCCCCA
251 GCATACACCT TCTTTTTTTT CTGGACACTT GGGAAAATAT AACTTTTTGA
301 TGTAGAACTC AAAATATTAG CCCAATAATA ATATTTAACA TCAACCAGCC
351 TCCTCTCATT TAATTCTCAC AACAGAATCT ATGAGTTGAG TGCAAAAATC
401 ATCCCTATTG TGCAGATGGG AAAACTGAGG GTCAGAAAAG TGAACCTCCC
451 AAGAACTGTC AAAGTTGGGA TTTGAACCCA GGTCTCTGAT GACTGGATGA
501 AGGAATGAAG ATACCTATAC TTGGGAATGA GGAGGGTCGA CAGGACACGA
551 GGGCTGACTT TGTATATTTT TAAACTTCAA AGATTTTCTG TATTTTCAGCT
601 GGGAATATGG TAGAAGGTTA ATTGGAACAA AAAAATGCAA AGCAATGAAT
651 AAGACCTCAG TATTTGCTAT GCACAACAGG GTGACTGTAG TCCCACAAAT
701 AACTTCACTG TACATTGTTA AAATATAACT AAAGGTGTAT GCTTGGATTG
751 TTTGCAACAC AAAGGATATA TGCTTGAGGG GATGGATACC CCATTTACCC
801 TGATGATTAT TATGCATTAC ATGCTTGTAT CAAAACATCT CATATACCCC
851 ATAAATATAA AAACACCTAC TATGTACCCC AAAAAATTAA AAACAAATAA
1051 AGGCATGGTG GCACACACCT GTAGTCCCAG CCACTCAGGA AGCTGAGGTG
1101 GGAGGATCGC CTGAGCCTAG GAGGCTGTAC TCCAGCCTGG GTGACAGAGC
1151 GAGACTCTAT CTCAAAAAAT AAAATAAAAT AATAAAAAGT AGAAATCAAG
1201 AGGGAAAATG TGGGAGAAAT TGGGATAATT TTAACAATAC CTTCCACCAG
1251 AGTGATGATG AAGAATGCAT AAGTCACTTC TTAGTGGTCT TGATCTATAA
1301 AAAGTGTTCA ATAAATATCG ATTATTGTTA CTGTTATTGC TTCTAGACGT

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Table 3 (continued)

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**Genomic Carboxy Terminal**  
**(SEQ ID NO: 3)**

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1351 AATTCCTGGA AGCATTTTTT TTTTTTTTTT TTTTGAGATG GAGTCATGCT  
 1401 CTGTTGCTCA GGCTGGAGTG CAGTGGTATG ATCTCGGCTC ACTACAACTG  
 1451 CCTCCTGGGT TCAAGCAATT CTCCTGCCTC AGCCCCCAT GTAGCAGGGA  
 1501 CTACAGGCAT GCGCCACCAC ACCCGGTGAA GTTTTGTATT TTTATTAGAG  
 1551 ACAGGGTTTT GCCATGTTGG TCAGGCTGGT CTCGAACTCC TGACCTCAGG  
 1601 CAATTTGCCT GCCTCGGCCT CCCAAAGTGC TGAGATTACA GGCTTGGGCC  
 1651 ACTGCATCCA GCCGAAGGCC TCCCATTTTG ATCAGAACCC TTCTCTAGAC  
 1701 TGAGGGTGGG TGCCTCTAGA TCTTTTGCTC TTTAAAGACA GCAACCGATG  
 1751 ACCCTGCTGA TGCTGAGTAC TGGCTGAATT CCTGTGGTCT CTGTCCCTAG

**Exon C2**

1801 GATGGACTCC GTGTGGTCA CTGTCAAGGC ATTGTTCTCC TCCAATTGG  
 1851 ACCCAGCCT GGTGGAGCAA GTCTTTCTAG ATAAGACCCT GAATGCCTCA  
 1901 TTCCATTGGC TGGGCTCCAC CTACCAGTTG GTGGACATCC ATGTGACAGG  
 1951 TACAAGGTGG GGTGGCTGGT TTCCTAACTG GAAGAGGTGG GGTTATGAGG  
 2001 AAAGATGGGG CTTCTCGGTA CCAGTGGAAAT TGGTGGAGGC TCTAGAGAGG  
 2051 GAAAGGGAGG CTTTCTGGAG ACCCATGTAG GTGACCTCTG GCAGTAGATC  
 2101 ATCCAACGAG GCAGGAACAG AACACCAGCC ATTGCATCTA AGAGAATAGC  
 2151 TATTTTTTACA TGTA AAAAGA ATTGTGTTGA ATGAATGAAT CAATAGATCA  
 2201 TTTATTTTGA ATCAATTTAT TGATTCATTC ATTTAATTAA TGAATAATAA  
 2251 ATGATTCAGT ACATAATTGA TTAATTGATG TAATTGAGAA TTGATTTAAT  
 2301 TGATTAATTG ATCAATTAAA ATGATCAATT AAATGAATGA ATCAGTAAAT  
 2351 GAATAATTCA TTCAATCAAT AAACAATGGA AGTAGGCCGG GCATGGTGGC  
 2401 TCACGCCTGT AATACCAGTA CTTTGGGAGG CCCAGGCAGG CAGATCACGA  
 2451 GGTCAGGAGA TTGAGACCAT CCTGGCTAAC ACGGTGAAAC CCTGTCTCTA

Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)					
2501	CTAAAAATAC	AAAAAAAATT	AGCCAGGCAT	GGTGGTGGCC	ACCTGTAGTC
2551	GCAGCTACTC	GGGAGGCTGA	GGCAGGAGAA	TGGCGTGAAC	CCGGGAGGCA
2601	GAGCTTGCAG	TGAGCCGAGA	TCGCGCCACT	GCACTCCAGC	CTGGGCGACA
2651	GATGGAGACT	CTGTCTCAAA	AATAAATAAA	TAAATAAAAA	TAAAAAATAA
2701	ATAACAATG	GAAGTAAACA	CGTACTGATA	ACACAGTGTG	ATCATTGCTA
2751	TGATAAGGGA	ATTTTCAGGGG	CCTGTGGGAG	CCCCAAGGAG	GAACACACAA
2801	CCTTGTCTTG	GAAAGTTTTA	TGTAGGAAGG	GGTGAAGAAG	CTGAGATCTG
2851	ACAGAGAATG	GGACCTAGCC	AGGGGTAATA	GATGGAGAAT	TGTGCTCCAT
2901	GCATCTATAA	CCTAGAAGAT	AGAAAGAATA	TGGCATCTGG	CCGGGTGCGG
2951	TGGCTCACGC	CTGTAGTCCC	AGCACTTTCA	GAGGCTGAGA	TGGGTGGATC
3001	ACCTGAGGTC	AGGAGTTCAA	GACCAGCCTG	ACCAATATGA	TGAAACCCCA
3051	TCTCTGCTAA	AAATACAAAA	ATTAGCCAGG	CATGGTGGTG	CGTGCCTGTA
3101	ATCCCAGCCA	CTTGGGAGGC	TGAGAGAGGA	GAAGTGTGTTG	AACTCGGGAG
3151	GCGGAGGTTG	CAGTGAGCCG	AGATTGTGCC	ATTGCACTCA	AGCCTGGGCA
3201	AAAAGAGCAA	AACTGCATTT	CAAAAAAAA	AAAAGTGGCA	TTTTGGGGCA
3251	AGTTTAAGAA	GATTGGTGTA	GCTGGAGCAT	CCACTTTGAT	ACTGGAGAGG
3301	TGACAGTTGA	AGCCAAAGAT	GTGGGCAGAG	ACTTTGTTGG	GCACTGGAAT

Table 3 (continued)

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**Genomic Carboxy Terminal**  
**(SEQ ID NO: 3)**

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3351 GGCTTGGGGA GGAACATGAC AACTCATGA GTTCTGCTTT AGAAAGAAAA  
 3401 TGAAATGAAT TCTGCTCATC CTCTGGGTGC TGTGTGCAGA ATGGAGGGTG  
 3451 GGGGGAGAGA AGAGCAAAGG CAAGAAGACC CTTTAGGAAC AATGATCATT  
 3501 AGTTAGAAGA CTCTGGGTTT CTCAGCACCT GCAATTGCTG ACTACACCCC  
 3551 CAGAGAAACC CAGTCTCTTT TCCCCATGT TGTAGAGAAT TCTTACAATG  
 3601 CTTGGTAGAA AGAGAATTGA ACAGGTAGAT GGGTGGATGG ATACAAGCTG  
 3651 GACAGATGGA TGGAGGAAGA TCCTCCATCC AATATAGAGC TGTTACCTAA  
 3701 AACCTCCAT CCCACCTTTA AAATCCTAGC TCAGCCAGGC GCGGTGGCTC  
 3751 ACACCTGTAA TCCCAGCACT TTGGGAGGCC AAGGCGGGTG GATCACTTGA  
 3801 GGTCGGGGGT TCGAGACCAG TCTGACCAAC ATGGTGAAAC CCCCTTCTCC  
 3851 ACTAAAAATA CAAAAAAAAA AAAAAGTTAG CCAGGCAGGG TGGCGCATGC  
 3901 CTGTAATCCC GCTACTCGGG AGGCTGAGGC AGGAGAATGG CTTGCACCCA  
 3951 GGAGGTGGAG GTTGTGGTGA GCCAAGATCA CGCCATTACA CTCCAGCCTG  
 4001 GGCAAAGAGA GTGAAACTGT CTCAAAAAAC AAAACAAATG ACCCCCCTGC  
 4051 CAAAAAAAAA AAAAAAAAAA AAGAAAAGAA AAAAAGAAAA GCCTAGCTCA  
 4101 GCTCACACTG TCAGGAATAA GTAAGCTAGC TGGAATCATC TCTTTCTTAA

**Exon C3**

4151 AACCTGCCT TGATAGTGA TTTTACATA CTTTTTTTTT AATTCTAGAA  
 4201 ATGGAGTCAT CAGTTTATCA ACCAACAAGC AGCTCCAGCA CCCAGCACTT  
 4251 CTACCTGAAT TTCACCATCA CCAACCTACC ATATCCCAG GACAAAGCCC  
 4301 AGCCAGGCAC CACCAATTAC CAGAGGAACA AAAGGAATAT TGAGGATGCG  
 4351 GTGAGAAGGG GGTGGTATGT CCACTCTGTT GCCATGCAGA AACTGACTTA  
 4401 TGCATACTGG GTAGCCACAG GGTGACTTTT TATAACAATC CACAAAGACA

Table 3 (continued)

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**Genomic Carboxy Terminal**  
**(SEQ ID NO: 3)**

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4451 GGTTCCTTATT CCCATTTAAT ACACAAGCAC AGAGAGGTTT AGTAGCTGAC  
 4501 CCAAGGTCAC ACAGCTAAGT CATACCCTAG AAGAGCATGT CCTTTGATAT  
 4551 ACATACCTGG GCAAGTGGTT GTCATGACAA GAAGCAAAAT AGACGGAGAA  
 4601 GTGTGCTCAG TGGCTGAAAA TTCTCTGATG CTAAGGGGGC CAGGATTCTG

**Exon C4**

4651 ACCTAAGAAA CATCGCCCTG TCTTTCAGCT CAACCAACTC TTCCGAAACA  
 4701 GCAGCATCAA GAGTTATTTT TCTGACTGTC AAGTTTCAAC ATTCAGGTAA  
 4751 GTTCTAACTC AGGACCTAAT GACTCTAGGA ACTTCTGCTG TCCTTTAAAT  
 4801 AGAAGTGTCC CCAAGCCATA GCTTTGATGG AAGAGAGCCC TAGAAATAGA  
 4851 GAGCTGTTAA CTAAAACTA GCTTTTTCCT AAAGCTGGAG CCCAACTGGC  
 4901 TTCAACACTC AAGAGAGCTG GTGTAAATCT CAGCAGACAT AAAGGTACCT  
 4951 GGTGCTGAGG CCATGGAGTC TAGAGTGTAG AATCTACTAC ATTAAGACAT  
 5001 CAGCTACTGA AATCAGGACC CATGGAAGAC GGGGGAAGGA GGGGACTAAA  
 5051 ACCAGATTAC TTAGAATCTA GCAGCCTAAC TGTGCTTTTC AATGAGAGGT  
 5101 ATCATTTCCA ATGGTGGGGG GTACCAATGA TTTTTTTTTT TTGACAACTG  
 5151 CCTTGAGAAC AGGCTTTCCT CACTAAACAA ATTCTGAATC AGAACAAATA  
 5201 AAGATAAGCC CTGAGAATAG GGCTTTTTTCA AGGAGCTGCC AAACAGATCA  
 5251 AATAGTGACT ATGTTCTGCA GATTGATGTC TGGAGAACTC TACAGCTATT  
 5301 TTGACTGCTA GGCAGCTGGT TTTCACAGAT ATCATGATTC TGAGGCTGCC  
 5351 AGTTTTTCAA GTTACCGAGG ATCTTGCTGG ATGCAGTGGC TTGCGACTGT  
 5401 AATCCCAGCC CTTTGGGAGG CCAAGGTGGG TAGATCGCTT GAGCTCAGGA  
 5451 GTTTGAGACC AGCCTGGGCA ATATGGTGAA AACCCATCTC TACAAAAAAT  
 5501 ACAAAAATCA GCTGAGCATA GTGGCATGTG CTGTAGTCCC AGTTACTTAG



Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)					
5551	GAGGCTGAGG	TGGGAGGATG	GCTTGAGCCC	AGGAGGCAGA	GGTTGCAGTG
5601	AGCTGACATT	GTGCCATGCA	CTCTAGCCTG	GGCAACAGAG	CCAAAGCCTG
5651	TCTCAAAAAA	AAAAAAACAA	ATAATAATAA	TAATAAAAATA	CTGAGGATCT
5701	TGAAAGAGCA	CTGTGGAAAT	AATGCAAGTT	AAAATGCCAC	AAAGCTTGCT
5751	CTTTTACTG	AGATTTAACA	CTTTCCTTAA	CTAAACACCC	CTCGAATTTT
5801	TGCAAGCCTT	TGGTTCACCT	CTAGACTTCT	GGAAAAATTG	ATTTGGACTA
5851	TTTGGCCAA	TGTTCTCATT	GATTTTATGG	GTATTCAGAA	GTTGTTACCC
5901	CAACATTCCA	GAAATGTTCT	CCCTGTGGCT	ATTACTTTAT	TTATTTATTT
5951	ATTTATTTAT	TTATTTATTT	ATTTGAGACG	GAGTCTCCCT	CTGTTGCCCA
6001	GGCTGGAGTG	CAGTGGCGCA	ATCTCAGCTC	ACTGCAACCT	CCGCTTCCCA
6051	GGTTCAAGCG	ATTCTCCTGC	CTCAGCCTCC	CAAGTAGCTG	GGATTATGGA
6101	TGTGCACCAC	CACACCGGCT	AATTTTTGTG	TTTTTAGTAG	AGATGGGGTT
6151	TCACTGTGTT	GGCCAGGCTG	GTCTCGAACT	CCTGATCTCA	AGTGATCCAC
6201	CCGCCTTGGC	CTCCCAAAGT	GCTGGGATAA	TAGGCATGAG	CCACTGTGCC
6251	TGACCTCCCT	GTGGCTATTT	TTAAATGAAT	TAAGTGGAAT	AAAATTAGAA
6301	ATTCAGTTCT	TCTCCCACGC	TAGCTGCATT	TTAAGCATTT	AATAACAACA
6351	TGAAGCTACT	AATGGCTGCA	TTGTGTAGTG	CAGATGTAGA	ATTTTTTTTT
6401	TGTTTTTTGT	TTTGTTTTTG	AGATGGAGTC	TCGCTCTGTC	ACCAGGCTAG
6451	AGTGCAGTGG	CGTGATCTCG	TCTCACTGCA	ATCTCTACTC	CCCGATTCAA
6501	GTGATTCTCC	TGCCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGCACGTGC
6551	CACCACACCC	AGCTAATATT	TGTATGGATG	GTCTCAATCT	CCTGACCTCG
6601	TGATTTGTAT	GGATGGTCTC	GATCTGACCT	CATGATCCGC	CTGCCTGGGC
6651	CTCCCAAAGT	GCTGGGATTA	CAGGCGTGAG	CCACTGTGCC	CGGCCGACAT
6701	AGAATGTTTA	CATCATTGCA	GAAAGTTTCT	GCAGGAAGAG	CCTAGAAGGA

Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)	
6751	GAAAGCCTAG AATCATGATA AAATTGCAGA TATCTTTGCT TATCCCTGTC
<b>Exon C5</b>	
6801	CCCTTCCAGG <u>TCTGTCCCA</u> ACAGGCACCA CACCGGGGTG GACTCCCTGT
6851	<u>GTAATTCTC</u> GCCACTGGCT CGGAGAGTAG ACAGAGTTGC CATCTATGAG
6901	<u>GAATTTCTGC</u> GGATGACCCG GAATGGTACC CAGCTGCAGA ACTTCACCCT
6951	<u>GGACAGGAGC</u> AGTGTCTTG TGGATGGTAA AGCTCCCTGG GTCATTGGGA
7001	CTGAGGTGGA AGCTCCCACT TCCTCACCTG GGTCTTCCC TGGGAATCTG
7051	AAGGCTTGGG GTTGATTCTG CATCGAGCTT TCTCAGACTG GGAGAAAGTG
7101	GCTTAGTTCT CCTAAGCTTT ACCCATCATT GAAGGAAAGA AAAGGACGCC
7151	CGAGGGATAT GGGAGGCATT TGCCCTCTTC TGGCCAGCTC TGTGACCTCA
7201	GGCTAGTCAC ATCTCCTTTC TGGACTTCTT ATCTCTCTGT ACTTAGCAAG
7251	CCACTTGGTT TTTGGTTCCC ATCTTGCCCTG CCCTAGATGG TATTGCTCCT
7301	CCACCCCCAG GCAGCTGCAG TGTAAACAA TTACCCTGAT TAGTTATTGT
7351	TGTTGTGTTG TTTGTTTGT TTTGAGACAG GGTCTCACTC TGTCACCTAG
7401	GCTGGAGTGC AGTGACATGA TCTCAGCTCA CTGCAACCTC AACCCCTGGA
7451	CTCAAGCAAT CCACCCACTT CAGCCTCCCA AGTAACTGGG ACTACAGCCA
7501	TGCGCCACCA CACCCGATA ATTTTGTAT TTTTCTAGA GATGGGGTTT
7551	TGCAACATTG CCCAGGCTGG TCTTGAACTC CTGAGCTCAA GCATGCCACC
7601	TGCTTCAGCC TCCCAAAGTG CTGGGATTAC AGGCAGGCAG GCACCACTGC
7651	AGCTGGTTCT GGTTTTTTGT GTTTGTTTTT TTCTTTTAGA GGCAGGGTCT
7701	CGCTCTGTTA ACCAGAATGG AGTACAGTGG TGCAATCATA GCTCACTGCA
7751	GTCTTGAACCT CCTGGGCTCA AGCGATCCTC CCACCTCAGC CTCCTGAGTA
7801	CCTGGAACTA CAGGCACGTG TCACCACGCC TTGCTAATTT CTAAATTTTT
7851	TGTAGAGACA GGGTCTCACT ATGTTGCCCA GACTGGTCTC TAATTCCTGG

Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)					
7901	CCACAAGTGA	TCCTCCTGCC	TCAGCAGGTC	AATGAGGGCT	TCCAGTTTCA
7951	AGTTGTATGT	GATTCATCCT	CAACAAATGT	GGTAGGATGG	ACCTATTTTC
8001	CAACTCCAGA	GATGGCTTCA	AGGTGGCTCA	ACTTTGCATA	TCCAATTTTA
8051	CCCATTCAAA	GAATAGTTAT	ATACATTGTA	CCATGTATCA	GGAATATAAC
8101	AGAGAGTAAC	TGTTTGCTCT	TTCACCACTA	TATTCCAAGA	ACCCCATATT
8151	CTGCCTGGCA	CATAATAAAC	ACTCAAGTCA	TATTTGCAGA	AGGAATAACT
8201	AGATTTCATA	CAAGGTTCTT	TTCAAGTCAA	ATGCGAATAA	CGTTTTAGAC
8251	GGGACCTTCC	AATGCCTGTG	TGCACTGTCC	TTGATTCCGA	ATTATTGTTG
8301	TGCAAGAGAG	CACTGTTGAT	CCTTCAGAAT	CAACAAGCCT	TTCACATGCC
8351	TGTCACAGGT	TTTTCTTTTT	CTTGTTTTAC	CAATTTTGTT	TGTTGTTTGT
8401	TTGTTGTTAT	TGTTTTGTTT	TGTTTTTGTT	TTTTATTGT	TTTTATTTTT
8451	TCTTTTTTTT	TGAGACAGAG	TCTCGCTCTG	TCACCCAGGC	TGGAGTGCAG
8501	TGGCAGGATC	TCCGCCCACT	GCAAGCTCCG	CCTCCTGGGT	TCATGCCATT
8551	TTCCTGCCTC	AGCCTCCTGA	GTAGCTGGGA	CTACAGGCGC	CTGCCACCAT
8601	GTCTGGCTAA	TTTTTTTTGT	ATTTTITAGTA	GAAACAGGGT	TTACCATGT
8651	TGACCAGGAT	GGTCTCGATC	TCCTGACCTC	GTGATCTGCC	CACCTGGGCC
8701	TCCCAAAGTG	CTGGGATTAC	AGGCGTGAGC	CACCACACCC	AGCCCCAATT
8751	TTTTTTTTTAA	TTAAAATTGT	TGTCAGCTCA	CAAGCTTTCT	AAAAACAGGC
8801	CATGGACCCA	GCATCGCTGT	AGTTTGCCAA	ACCCTTGCTT	TGAATCAGTA
8851	CCATCCAATA	GAACTTTCTG	CAGTGATAGA	AAATGTTTCT	ATCTGTGCTA
8901	TTCAGCACAA	AGCCATGTGT	GATTACTAAG	CTTGAAGTGT	GGTTAATGTA
8951	ACTGAGATAC	CGAAGTTTTA	ATTTTATTTA	ATTTTAATTT	AAAAAGCCAC
9001	TTGTGGCTGC	TCCATATTGC	ACACTACTTT	TTAAAATTAT	TATTTGTATA
9051	TATTTAAGGG	GCACAAGTAC	AATTTTGTTG	CATGGATTTA	TAGCCAGTG

Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)					
9101	GGGAAGTCTG	GGCTTTTAGG	GTATCTATTA	CCTGAATAAT	GTACATTGTA
9151	CCCATTGAGT	AATTTCTCAT	CATCCACTCT	CCTCCACTCC	CCAACCCCTC
9201	CAAGTTTCCA	CTGTCTATTA	TTCCACTCTC	TATGTCCATG	CCTATGCATT
9251	ATTTAGCATT	GACATGTCTA	TGCATTATTT	AGTCAAATAC	ATGTGCTATT
9301	TGACTTCCTG	TATCTGAGTT	GTTTGACTTA	AGATAATGAC	CTTCACTTGC
9351	ATCCATGTTG	CTGCAAAAGA	CATGATTTCA	TTCTTTTTTTA	TGCCTGGGTG
9401	GTATTGCATT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTAGAG	AGAGAGAGAG
9451	ATCACATTTT	CTTTATACAG	TCCTCCATTG	ATGGGCACTT	AGGTTGATTG
9501	CATATCTTTG	CTATTGTGAA	TAGTTTGTGT	ATAAACACAC	AGGTTGAGGT
9551	GTCTTTTTGA	CAAATTATT	TATTTTCCTT	TGTGTAGATA	CCCAGTCGTG
9601	GGATTCCTGG	ATCAAATGGT	AGTTTCATTT	TTAGTTATTT	GAGAAATCTC
9651	CACGTTTTTC	ATAGAGATTA	TACTAAATTA	CATTCCCACC	AACAGTGTGT
9701	AACGGTTCAC	TTTTCTTGCA	TCCTTTTTTAA	CATCTGTTAT	TTTTGTCTTT
9751	TTAGTAACAG	CCATTCTGAC	TGGCGTAAGG	TGGTATCTCA	TCATGGTTTT
9801	AATCTGTATT	TCTCTGATTA	TTAGTAATGT	CGAGCATTTT	TTCATATGCT
9851	TGTTAGCCAT	TGGTATGTCT	TCTACATCTT	TAAGAAGCTG	GCTATGGGCT
9901	GGGCGCAGTG	GCTCACACCT	GTAATCCCAG	CAC'TTTGGGA	GGCCGAGGCA
9951	GGCGGATCAC	GAGGTCAGGA	GTTAAAAACC	AGCCTGGCCA	ACATGGTAAA
10001	ACCCTGCCTC	TACTAAAAAT	ACAAAAAATT	ACCCAGGCAT	GGTGGTGCGC
10051	CTGTAATCCC	AGCTACTCAG	GAAGCTGAGG	CAGGAGAATC	ACTTGAACCC
10101	AGGAGGCGGA	GGTTGCAGTG	AGACGAGATC	ACATCATTGC	ACTCCAGCCT
10151	GGGTGACAGA	GTGAGACTCT	ATCTTGAGAA	AAAAAAAAAG	TTGGCTATAA
10201	CAGGGTTGTA	GAAGTAGAGG	AACCAGTAAC	CCTTCTCGCC	ATGCCTGATG
10251	ATGGCTTTAC	ATCCCTGTCT	TCATGGAGTT	TATGCTGTCTG	TGAGGAATAA

Table 3 (continued)

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Genomic Carboxy Terminal  
(SEQ ID NO: 3)

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10301 CAAGAACAGG CAGTTGTCAA TTATAAATTA TTTGATGTGA ACCTATTCAT  
 10351 ACATGGGTGT GGTCA TCAGG GAAGGCTTCC TGGAGGAAAT GACATTGAAG  
 10401 GTGAATTCTA AAAGATGACG ATAAACCACC AAGTGAAGGA GAGCTTAAAT  
 10451 GTGTTTTTAG GCAGAAGAAA AACCTTTTGG GTGAAAATTT TAAAACTTAG  
 10501 AGAGGTCCCA TCAGTTTCCA ACTGCGATGA TCCATTCTCT CCACCACTGC  
 10551 CCTTGGGCCC AGCCCAATTT AGGTCCACCA TGCCCAGAGG CATGAATTTA  
 10601 ACTTATGACA CTCTTG TGGT GGAATAATGG CTTTGGGCTT ATGTAGCCAT  
 10651 GTGTCATTTT TTTAGAGATA CAAATTGAAA TATTTGGGGT GAGATGTCAT  
 10701 GGTGTCTACT GGCCTCTAAA ACTTCAGTGA AAACATTTAC TTTCCTGAA  
 10751 ATGTCAATAA ATCATAAATT GGATGTATAT GTTTTAGTTG GAGGAAATAT  
 10801 AAACCACTAA ATCTAGGTGA TGCATATTTA TTATACTCTT CTCTCTGCTT  
 10851 TTTTGTACGC TTGTAAAATT GTATTTAAAA GAATAAGACA CACTTGCCCG  
 10901 GGC GCGGTGG CTCACGCCTG TAATCCCAGC ACTTTGGGAG ACCGAGGTGG  
 10951 GTGGATCATG AGGTCAGGAG TTCAAGACCA GCCTGGCCAA CATGGTAAAA  
 11001 CTCCATCACT ACATACAAAA ATTAGCCAGG CATTTTGGCG GGCACCTGTA  
 11051 ATCTCAGCTA CTTGGGAGGC TGAAGCAGGA GAATTGCTTG AACCCGGGAA  
 11101 GCAGAGGTTG CAGTGAGCCA AGATCACGCC ACTGCACTCT AGCCTGGGCA  
 11151 ACAGAGCAAG ACTCCATCTC CAGAAAAAAA AAAAAAAAAA GACACACTCA

**Exon C6**

11201 CATGCACCCT CCATTTCTTT CATTTCTAGG GTATTCTCCC AACAGAAATG  
 11251 AGCCCTTAAC TGGAATTCT GGTAAGTCTC AAAGAAGCCC CAGCCCAGGG  
 11301 TAGGGAGGGG GTAGCCTGAT GGTGCTTTGC CTTGTCCAAG AGCACCAGGC  
 11351 ACACAGAGTC TTGGATGAGG ATCAAAATTG CCAACCCATG GCAAAGACTA  
 11401 TTGAGGCATA GTAAAGGGAT AGCAGGGATC CTGGCTTTCT GGGGGCCCAG

Table 3 (continued)

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Genomic Carboxy Terminal  
(SEQ ID NO: 3)

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11451 TTTTGGGGG CATCAGAGGC ATGAGGTGTT GAGCCACTAA GCTCTCTTCC

11501 CCAGGGGCTG TGCCCATCCT CAGGCCACAT AGGGTCCAAG AAGGAGCCCT

**Exon C7**

11551 GGGACGTGGC AGGAGGTGGC TCACCCAGC CCTTGTCTCC CCAGACCTTC

11601 CCTTCTGGGC TGTATCCTC ATCGGCTTGG CAGGACTCCT GGGAGTCATC

11651 ACATGCCTGA TCTGCGGTGT CCTGGTGAGC AAGGAAGGGT TGCTTGTCTT

11701 CTTAACAATT GGGTTGTAAG AGTTCTTAAT ATATTATAAA ACCATACTAT

11751 ACTATACACA AGTCCTTTGC TGGATATATG TTTTGCAAAT ATTTTCTCCC

11801 AGTTCACGGA GTGGCTTTCC TATTTTCTTT TTATAATTTT ATTTTAAATT

11851 AATTGACAAA TAATGAATGC ATATATTTAG GGGATACAAAT GTGATGCTTT

11901 GGTATATGTA CAATTATGGA ATGACTCAAT CAAGCTAATT AATATGTCCC

11951 TCACCTCTCA TACTTATTAT TTCTTTGTGG TGTGAACATT GGCAACCTAT

12001 ACTCTTAGCA ATTTTGAAAT CTACATTATT ATTAACATA GTTACTATGT

12051 TATGCAGATC TCAAAAACCTT CACAACCTAT ATGCTGATTA CAAGATATTG

12101 AGAGAAAAAG TGATTGCAAA GAGTGTAAT AAAATAATGT AAGAGGGAAA

12151 AATGTAACAA AATTAGTCGT TAGGGAAATG TACACGGAAG TCACAATGAG

12201 AGGCCACTTT TCACAAGAAT GGATAAAATT GAAAAGATTG ACTATAACAA

12251 GTGTTGGTGA AAATGTGACA GAACTGGAAC TCTCATAAAG TGAAAGTGGA

12301 AAATAGCTTG GCCATTTCTT TGAAAATTAC ACACACCTAC CGTAAGACCT

12351 ACCATCCAC TACTAGTAAT TTATCTAAGA GAAATAAAAA CATATGTCTA

12401 TATGAAGACT TGTACACAAG TAAATGTTCA TAACAGCTTT GTTTGTAATA

Table 3 (continued)

		Genomic Carboxy Terminal (SEQ ID NO: 3)				
12451	GCCAAACTCT	GAAAACAAGC	CCCTAATGTC	CATTAACAAA	TATATCCTGA	
12501	CAATGGAATA	TTATTTCAGCA	ACAAAAAGGA	ATTATTAATA	CATTAATAAA	
12551	TTATACAGCA	ACATGTATAA	ATTGCAAAAT	AGTTATGCCT	AGTGAAAGAA	
12601	TCCAGATGAA	GAAAAGAGTA	CATGCCATAT	GATTCCCTTA	ATAGACAAAT	
12651	TCTAGAAAAT	ACAAACTAAT	CTGTAAGGAC	AGGAATCAGA	TCAGCGGTTG	
12701	CCTGGGAATG	AAAATGTGTT	TGCAGTGGCA	GGGAAAAAGG	AATTGTAAAA	
12751	GAGCAGGAAG	AAAGTTTTTT	TGTTGTTTTT	TTTTTGTTTT	TTCTTGAGAC	
12801	AGAGTCTTAG	TCTATCGCCC	AAGCTGGAGT	GCAATGGCAC	GATCTCAGCT	
12851	CATTGCAACC	TCTGCCTCTC	GGGTTCAAGC	GTTTTTCCTG	CCCCAGCCTC	
12901	CCAAGTAGCT	GGGATTACAC	ATGCGCACCA	CCACACTCAG	CTAATTTTTG	
12951	TATTTTTAGT	AGAGACGGGG	TTTTACCATG	TTGGCCAGGC	TGGTCTCGAA	
13001	CTCCTGACCT	CAGGTGATCC	ACCCGCCTTG	GCCTCCCAA	GTGCTGGGAT	
13051	TACAGGAGTG	AGCCACCATG	CCTGGCCAGG	ACGAAAGTTT	TGGGGATGAT	
13101	GGATGGATGT	TCCTTATGTT	GATTGTGGTG	ACGATTCAAT	AAGTTATGAT	
13151	CAGAACTTAT	CAAAACATTC	ACTTTAAATG	TGTGCAGTTT	ATTTTATGTC	
13201	AGTTATGCCT	CAGTTAAGCT	GGACAGATGT	AGAGGAGGAA	GGGAGGGAGA	
13251	GAGGGGGCTG	AGATCAGGAC	CAAAGCCAG	AGAGAAAGAG	ACTGAGAATG	
13301	AGATGAGAGA	GAAATGGTAT	TTAGACAGAA	GACAGGCGAT	AGATGATTGA	
13351	TAGTTGACAG	ATGATTGGTG	GATANNNNNN	NNNNNNNNNN	NNNNNNNNNN	
13401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	

Table 3 (continued)

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**Genomic Carboxy Terminal**  
**(SEQ ID NO: 3)**

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13451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
 13501 AGGAGGTTTA AACAAAACGC AATTATGTTG AAATGACAAT GATTGTGGAT  
 13551 ATAAAGGTAG ATAGAAATAG ATATTTGTGA AGATAATGGT TAGATAAAAA  
 13601 TGATAGGTAA CAGATATTGA TAGATCTTGA TAAGTAGATG ATAAATACAT  
 13651 GATTGATGGA TGACAGGTGA TTGATAGATG ATTTGATGGA TTATAAATAG  
 13701 GAGATGATTG AGAGGTGAGA GATAATTGAT GGTATTATTGA TTGGTAGATA  
 13751 ATTGATTGAC AGGTTGATAA ATATTGATAG CTAGATGATA GATAAATAGA  
 13801 TCATTGGTAG ATATGTGATA TATTGATAAA GAAATTCAGA GGCAAAAGGA  
 13851 GAGAGAAATG AAGGGGATAT CGGAGGGGGA AAAATTTTTT TAAACCGAGA  
 13901 GTGAAACAAG GAGACAGAAG AAAAGAAAGT GGTGAAAAGA GGAAAAGAAC  
 13951 TGAGGGAGAA ATTAAATGAA ACAATGAAGG GAGACAGAGG AAGCATAAGG

**Exon C8**

14001 CCTCTGGCTT TGGCCATATT CTCACCCCTG TGGTCTCCTC TCCCTGGACG  
 14051 GCTGACCAGT CCATTCTCAC GCCTCCTCCT CACCCTCATA GGTGACCACC  
 14101 CGCCGGCGGA AGAAGGAAGG AGAATACAAC GTCCAGCAAC AGTGCCAGG  
 14151 CTACTACCAG TCACACCTAG ACCTGGAGGA TCTGCAATGA CTGGAACCTG  
 14201 CCGGTGCCTG GGGTGCCTTT CCCCAGCCA GGGTCCAAAG AAGCTTGGCT  
 14251 GGGGCAGAAA TAAACCATAT TGGTCGG



Table 4

Human cDNA of CA125 (SEQ ID NO: 4)					
1	AAGCGTTGCA	CAATTCCCCC	AACCTCCATA	CATACGGCAG	CTCTTCTAGA
51	CACAGGTTTT	CCCAGGTCAA	ATGCGGGGAC	CCCAGCCATA	TCTCCCACCC
101	TGAGAAATTT	TGGAGTTTCA	GGGAGCTCAG	AAGCTCTGCA	GAGGCCACCC
151	TCTCTGAGGG	GATTCTTCTT	AGACCTCCAT	CCAGAGGCAA	ATGTTGACCT
201	GTCCATGCTG	AAACCCTCAG	GCCTTCCTGG	GTCATCTTCT	CCCACCCGCT
251	CCTTGATGAC	AGGGAGCAGG	AGCACTAAAG	CCACACCAGA	AATGGATTCA
301	GGACTGACAG	GAGCCACCTT	GTCACCTAAG	ACATCTACAG	GTGCAATCGT
351	GGTGACAGAA	CATACTCTGC	CCTTTACTTC	CCCAGATAAG	ACCTTGGCCA
401	GTCCTACATC	TTCGGTTGTG	GGAAGAACCA	CCCAGTCTTT	GGGGGTGATG
451	TCCTCTGCTC	TCCCTGAGTC	AACCTCTAGA	GGAATGACAC	ACTCCGAGCA
501	AAGAACCAGC	CCATCGCTGA	GTCCCCAGGT	CAATGGAACT	CCCTCTAGGA
551	ACTACCCTGC	TACAAGCATG	GTTTCAGGAT	TGAGTCCCCC	AAGGACCAGG
601	ACCAGTTCCA	CAGAAGGAAA	TTTTACCAA	GAAGCATCTA	CATACACACT
651	CACTGTAGAG	ACCACAAGTG	GCCCAGTCAC	TGAGAAGTAC	ACAGTCCCCA
701	CTGAGACCTC	AACAAC TGAA	GGTGACAGCA	CAGACCUC	CTGGGACACA
751	AGATATATTC	CTGTAAAAAT	CACATCTCCA	ATGAAAACAT	TTGCAGATTC
801	AACTGCATCC	AAGGAAAATG	CCCCAGTGTC	TATGACTCCA	GCTGAGACCA
851	CAGTTACTGA	CTCACATACT	CCAGGAAGGA	CAAACCCATC	ATTTGGGACA
901	CTTTATTCTT	CCTTCCTTGA	CCTATCACCT	AAAGGGACCC	CAAATTCCAG
951	AGGTGAAACA	AGCCTGGAAC	TGATTCTATC	AACCACTGGA	TATCCCTTCT
1001	CCTCTCCTGA	ACCTGGCTCT	GCAGGACACA	GCAGAATAAG	TACCAGTGCG
1051	CCTTTGTCAT	CATCTGCTTC	AGTTCTCGAT	AATAAAATAT	CAGAGACCAG
1101	CATATTCTCA	GGCCAGAGTC	TCACCTCCCC	TCTGTCTCCT	GGGGTGCCCG
1151	AGGCCAGAGC	CAGCACAATG	CCCAACTCAG	CTATCCCTTT	TTCCATGACA
1201	CTAAGCAATG	CAGAAACAAG	TGCCGAAAGG	GTCAGAAGCA	CAATTCCTC

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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1251	TCTGGGGACT	CCATCAATAT	CCACAAAGCA	GACAGCAGAG	ACTATCCTTA
1301	CCTTCCATGC	CTTCGCTGAG	ACCATGGATA	TACCCAGCAC	CCACATAGCC
1351	AAGACTTTGG	CTTCAGAATG	GTTGGGAAGT	CCAGGTACCC	TTGGTGGCAC
1401	CAGCACTTCA	GCGCTGACAA	CCACATCTCC	ATCTACCACT	TTAGTCTCAG
1451	AGGAGACCAA	CACCCATCAC	TCCACGAGTG	GAAAGGAAAC	AGAAGGAACT
1501	TTGAATACAT	CTATGACTCC	ACTTGAGACC	TCTGCTCCTG	GAGAAGAGTC
1551	CGAAATGACT	GCCACCTTGG	TCCCCACTCT	AGGTTTTACA	ACTCTTGACA
1601	GCAAGATCAG	AAGTCCATCT	CAGGTCTCTT	CATCCCACCC	AACAAGAGAG
1651	CTCAGAACCA	CAGGCAGCAC	CTCTGGGAGG	CAGAGTTCCA	GCACAGCTGC
1701	CCACGGGAGC	TCTGACATCC	TGAGGGCAAC	CACTTCCAGC	ACCTCAAAAG
1751	CATCATCATG	GACCAGTGAA	AGCACAGCTC	AGCAATTTAG	TGAACCCAG
1801	CACACACAGT	GGGTGGAGAC	AAGTCCTAGC	ATGAAAACAG	AGAGACCCCC
1851	AGCATCAACC	AGTGTGGCAG	CCCCTATCAC	CACTTCTGTT	CCCTCAGTGG
1901	TCTCTGGCTT	CACCACCCTG	AAGACCAGCT	CCACAAAAGG	GATTTGGCTT
1951	GAAGAAACAT	CTGCAGACAC	ACTCATCGGA	GAATCCACAG	CTGGCCCAAC
2001	CACCCATCAG	TTTGCTGTTC	CCACTGGGAT	TTCAATGACA	GGAGGCAGCA
2051	GCACCAGGGG	AAGCCAGGGC	ACAACCCACC	TACTCACCAG	AGCCACAGCA
2101	TCATCTGAGA	CATCCGCAGA	TTTGACTCTG	GCCACGAACG	GTGTCCCAGT
2151	CTCCGTGTCT	CCAGCAGTGA	GCAAGACGGC	TGCTGGCTCA	AGTCCTCCAG
2201	GAGGGACAAA	GCCATCATAT	ACAATGGTTT	CTTCTGTCAT	CCCTGAGACA
2251	TCATCTCTAC	AGTCCTCAGC	TTTCAGGGAA	GGAACCAGCC	TGGGACTGAC
2301	TCCATTAAAC	ACTAGACATC	CCTTCTCTTC	CCCTGAACCA	GACTCTGCAG
2351	GACACACCAA	GATAAGCACC	AGCATTCCTC	TGTTGTCATC	TGCTTCAGTT
2401	CTTGAGGATA	AAGTGTGAGC	GACCAGCACA	TTCTCACACC	ACAAAGCCAC
2451	CTCATCTATT	ACCACAGGGA	CTCCTGAAAT	CTCAACAAAG	ACAAAGCCCA

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
2501	GCTCAGCCGT	TCTTTCCTCC	ATGACCCTAA	GCAATGCAGC	AACAAGTCCT
2551	GAAAGAGTCA	GAAATGCAAC	TTCCCCTCTG	ACTCATCCAT	CTCCATCAGG
2601	GGAAGAGACA	GCAGGGAGTG	TCCTCACTCT	CAGCACCTCT	GCTGAGACTA
2651	CAGACTCACC	TAACATCCAC	CCAACTGGGA	CACTGACTTC	AGAATCGTCA
2701	GAGAGTCCTA	GCACTCTCAG	CCTCCCAAGT	GTCTCTGGAG	TCAAACCAC
2751	ATTTTCTTCA	TCTACTCCTT	CCACTCATCT	ATTTACTAGT	GGAGAAGAAA
2801	CAGAGGAAAC	TTCGAATCCA	TCTGTGTCTC	AACCTGAGAC	TTCTGTTTCC
2851	AGAGTAAGGA	CCACCTTGGC	CAGCACCTCT	GTCCCTACCC	CAGTATTCCC
2901	CACCATGGAC	ACCTGGCCTA	CACGTTGAGC	TCAGTTCTCT	TCATCCCACC
2951	TAGTGAGTGA	GCTCAGAGCT	ACGAGCAGTA	CCTCAGTTAC	AAACTCAACT
3001	GGTTCAGCTC	TTCCTAAAT	ATCTCACCTC	ACTGGGACGG	CAACAATGTC
3051	ACAGACCAAT	AGAGACACGT	TTAATGACTC	TGCTGCACCC	CAAAGCACAA
3101	CTTGGCCAGA	GACTAGTCCC	AGATTCAAGA	CAGGGTTACC	TTCAGCAACA
3151	ACCACTGTTT	CAACCTCTGC	CACTTCTCTC	TCTGCTACTG	TAATGGTCTC
3201	TAAATTCACT	TCTCCAGCAA	CTAGTTCCAT	GGAAGCAACT	TCTATCAGGG
3251	AACCATCAAC	AACCATCCTC	ACAACAGAGA	CCACGAATGG	CCCAGGCTCT
3301	ATGGCTGTGG	CTTCTACCAA	CATCCCAATT	GGAAAGGGCT	ACATTACTGA
3351	AGGAAGATTG	GACACAAGCC	ATCTGCCCAT	TGGAACCACA	GCTTCCTCTG
3401	AGACATCTAT	GGATTTTACC	ATGGCCAAAG	AAAGTGTCTC	AATGTCAGTA
3451	TCTCCATCTC	AGTCCATGGA	TGCTGCTGGC	TCAAGCACTC	CAGGAAGGAC
3501	AAGCCAATTC	GTTGACACAT	TTTCTGATGA	TGTCTATCAT	TTAACATCCA
3551	GAGAAATTAC	AATACCTAGA	GATGGAACAA	GCTCAGCTCT	GACTCCACAA
3601	ATGACTGCAA	CTCACCCTCC	ATCTCCTGAT	CCTGGCTCTG	CTAGAAGCAC
3651	CTGGCTTGGC	ATCTTGTCCT	CATCTCCTTC	TTCTCCTACT	CCCAAAGTCA
3701	CAATGAGCTC	CACATTTTCA	ACTCAGAGAG	TCACCACAAG	CATGATAATG

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
3751	GACACAGTTG	AAACTAGTCG	GTGGAACATG	CCCAACTTAC	CTTCCACGAC
3801	TTCCCTGACA	CCAAGTAATA	TTCCAACAAG	TGGTGCCATA	GGAAAAAGCA
3851	CCCTGGTTCC	CTTGGACACT	CCATCTCCAG	CCACATCATT	GGAGGCATCA
3901	GAAGGGGGAC	TTCCAACCCCT	CAGCACCTAC	CCTGAATCAA	CAAACACACC
3951	CAGCATCCAC	CTCGGAGCAC	ACGCTAGTTC	AGAAAGTCCA	AGCACCATCA
4001	AACTTACCAT	GGCTTCAGTA	GTAAAACCTG	GCTCTTACAC	ACCTCTCACC
4051	TTCCCCTCAA	TAGAGACCCA	CATTCATGTA	TCAACAGCCA	GAATGGCTTA
4101	CTCTTCTGGG	TCTTCACCTG	AGATGACAGC	TCCTGGAGAG	ACTAACACTG
4151	GTAGTACCTG	GGACCCCACC	ACCTACATCA	CCACTACGGA	TCCTAAGGAT
4201	ACAAGTTCAG	CTCAGGTCTC	TACACCCAC	TCAGTGAGGA	CACTCAGAAC
4251	CACAGAAAAC	CATCCAAAGA	CAGAGTCCGC	CACCCCAGCT	GCTTACTCTG
4301	GAAGTCCTAA	AATCTCAAGT	TCACCCAATC	TCACCAGTCC	GGCCACAAAA
4351	GCATGGACCA	TCACAGACAC	AACTGAACAC	TCCACTCAAT	TACATTACAC
4401	AAAATTGGCA	GAAAAATCAT	CTGGATTTGA	GACACAGTCA	GCTCCAGGAC
4451	CTGTCTCTGT	AGTAATCCCT	ACCTCCCCTA	CCATTGGAAG	CAGCACATTG
4501	GAACTAACTT	CTGATGTCCC	AGGGGAACCC	CTGGTCCTTG	CTCCCAGTGA
4551	GCAGACCACA	ATCACTCTCC	CCATGGCAAC	ATGGCTGAGT	ACCAGTTTGA
4601	CAGAGGAAAT	GGCTTCAACA	GACCTTGATA	TTTCAAGTCC	AAGTTCACCC
4651	ATGAGTACAT	TTGCTATTTT	TCCACCTATG	TCCACACCTT	CTCATGAACT
4701	TTCAAAGTCA	GAGGCAGATA	CCAGTGCCAT	TAGAAATACA	GATTCAACAA
4751	CGTTGGATCA	GCACCTAGGA	ATCAGGAGTT	TGGGCAGAAC	TGGGGACTTA
4801	ACAACTGTTC	CTATCACCCC	ACTGACAACC	ACGTGGACCA	GTGTGATTGA
4851	ACACTCAACA	CAAGCACAGG	ACACCCTTTC	TGCAACGATG	AGTCCTACTC
4901	ACGTGACACA	GTCACTCAAA	GATCAAACAT	CTATACCAGC	CTCAGCATCC
4951	CCTTCCCATC	TTACTGAAGT	CTACCCTGAG	CTCGGGACAC	AAGGGAGAAG

Table 4 (continued)

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**Human cDNA of CA125**  
(SEQ ID NO: 4)

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5001 CTCTCTGAG GCAACCACTT TTTGGAAACC ATCTACAGAC ACACTGTCCA  
5051 GAGAGATTGA GACTGGCCCA ACAAACATTC AATCCACTCC ACCCATGGAC  
5101 AACACAACAA CAGGGAGCAG TAGTAGTGGA GTCACCCTGG GCATAGCCCA  
5151 CCTTCCCATA GGAACATCCT CCCAGCTGA GACATCCACA AACATGGCAC  
5201 TGGAAAGAAG AAGTTCTACA GCCACTGTCT CTATGGCTGG GACAATGGGA  
5251 CTCCTTGTTA CTAGTGCTCC AGGAAGAAGC ATCAGCCAGT CATTAGGAAG  
5301 AGTTTCCTCT GTCCTTTCTG AGTCAACTAC TGAAGGAGTC ACAGATTCTA  
5351 GTAAGGGAAG CAGCCCAAGG CTGAACACAC AGGGAAATAC AGCTCTCTCC  
5401 TCCTCTCTTG AACCCAGCTA TGCTGAAGGA AGCCAGATGA GCACAAGCAT  
5451 CCCTCTAACC TCATCTCCTA CAACTCCTGA TGTGGAATTC ATAGGGGGCA  
5501 GCACATTTTG GACCAAGGAG GTCACCACAG TTATGACCTC AGACATCTCC  
5551 AAGTCTTCAG CAAGGACAGA GTCCAGCTCA GCTACCCTTA TGTCCACAGC  
5601 TTTGGGAAGC ACTGAAAATA CAGGAAAAGA AAAACTCAGA ACTGCCTCTA  
5651 TGGATCTTCC ATCTCCAAC CTATCAATGG AGGTGACACC ATGGATTCTT  
5701 CTCACTCTCA GTAATGCCCC CAATACCACA GATTCATTG ACCTCAGCCA  
5751 TGGGGTGAC ACCAGCTCTG CAGGGACTTT GGCCACTGAC AGGTCATTGA  
5801 ATACTGGTGT CACTAGAGCC TCCAGATTGG AAAACGGCTC TGATACCTCT  
5851 TCTAAGTCCC TGTCTATGGG AAACAGCACT CACACTTCCA TGA CTGACAC  
5901 AGAGAAGAGT GAAGTGTCTT CTCAATCCA TCCCCGACCT GAGACCTCAG  
5951 CTCCTGGAGC AGAGACCACT TTGACTTCCA CTCCTGGAAA CAGGGCCATA  
6001 AGCTTAACAT TGCCTTTTTC ATCCATTCCA GTGGAAGAAG TCATTCTTAC  
6051 AGGCATAACC TCAGGACCAG ACATCAACTC AGCACCCTATG ACACATTCTC  
6101 CCATCACCCC ACCAACAATT GTATGGACCA GTACAGGCAC AATTGAACAG  
6151 TCCACTCAAC CACTACATGC AGTTTCTTCA GAAAAAGTTT CTGTGCAGAC  
6201 ACAGTCAACT CCATATGTCA ACTCTGTGGC AGTGTCTGCT TCCCCTACCC

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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6251	ATGAGAATTC	AGTCTCTTCT	GGAAGCAGCA	CATCCTCTCC	ATATTCCTCA
6301	GCCTCACTTG	AATCCTTGGA	TTCCACAATC	AGTAGGAGGA	ATGCAATCAC
6351	TTCTTGCTA	TGGGACCTCA	CTACATCTCT	CCCCACTACA	ACTTGGCCAA
6401	GTACTAGTTT	ATCTGAGGCA	CTGTCCTCAG	GCCATTCTGG	GGTTTCAAAC
6451	CCAAGTTCAA	CTACGACTGA	ATTTCCACTC	TTTTCAGCTG	CATCCACATC
6501	TGCTGCTAAG	CAAAGAAATC	CAGAAACAGA	GACCCATGGT	CCCCAGAATA
6551	CAGCCGCGAG	TACTTTGAAC	ACTGATGCAT	CCTCGGTCAC	AGGTCTTTCT
6601	GAGACTCCTG	TGGGGGCAAG	TATCAGCTCT	GAAGTCCCTC	TTCCAATGGC
6651	CATAACTTCT	AGATCAGATG	TTTCTGGCCT	TACATCTGAG	AGTACTGCTA
6701	ACCCGAGTTT	AGGCACAGCC	TCTTCAGCAG	GGACCAAATT	AACTAGGACA
6751	ATATCCCTGC	CCACTTCAGA	GTCTTTGGTT	TCCTTTAGAA	TGAACAAGGA
6801	TCCATGGACA	GTGTCAATCC	CTTTGGGGTC	CCATCCAAC	ACTAATACAG
6851	AAACAAGCAT	CCCAGTAAAC	AGCGCAGGTC	CACCTGGCTT	GTCCACAGTA
6901	GCATCAGATG	TAATTGACAC	ACCTTCAGAT	GGGGCTGAGA	GTATTCCCAC
6951	TGTCTCCTTT	TCCCCCTCCC	CTGATACTGA	AGTGACAACT	ATCTCACATT
7001	TCCCAGAAAA	GACAACTCAT	TCATTTAGAA	CCATTTTCATC	TCTCACTCAT
7051	GAGTTGACTT	CAAGAGTGAC	ACCTATTCCT	GGGGATTGGA	TGAGTTCAGC
7101	TATGTCTACA	AAGCCACAG	GAGCCAGTCC	CTCCATTACA	CTGGGAGAGA
7151	GAAGGACAAT	CACCTCTGCT	GCTCCAACCA	CTTCCCCCAT	AGTTCTCACT
7201	GCTAGTTTCA	CAGAGACCAG	CACAGTTTCA	CTGGATAATG	AAACTACAGT
7251	AAAAACCTCA	GATATCCTTG	ACGCACGGAA	AACAAATGAG	CTCCCCCTCAG
7301	ATAGCAGTTC	TTCTTCTGAT	CTGATCAACA	CCTCCATAGC	TTCTTCAACT
7351	ATGGATGTCA	CTAAAACAGC	CTCCATCAGT	CCCACTAGCA	TCTCAGGAAT
7401	GACAGCAAGT	TCCTCCCCAT	CTCTCTTCTC	TTCAGATAGA	CCCCAGGTTC
7451	CCACATCTAC	AACAGAGACA	AATACAGCCA	CCTCTCCATC	TGTTTCCAGT

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**


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7501	AACACCTATT	CTCTTGATGG	GGGCTCCAAT	GTGGGTGGCA	CTCCATCCAC
7551	TTTACCACCC	TTTACAATCA	CCCACCCTGT	CGAGACAAGC	TCGGCCCTAT
7601	TAGCCTGGTC	TAGACCAGTA	AGAACTTTCA	GCACCATGGT	CAGCACTGAC
7651	ACTGCCTCCG	GAGAAAATCC	TACCTCTAGC	AATTCTGTGG	TGACTTCTGT
7701	TCCAGCACCA	GGTACATGGG	CCAGTGTAGG	CAGTACTACT	GACTTACCTG
7751	CCATGGGCTT	TCTCAAGACA	AGTCCTGCAG	GAGAGGCACA	CTCACTTCTA
7801	GCATCAACTA	TTGAACCAGC	CACTGCCTTC	ACTCCCCATC	TCTCAGCAGC
7851	AGTGGTCACT	GGATCCAGTG	CTACATCAGA	AGCCAGTCTT	CTCACTACGA
7901	GTGAAAGCAA	AGCCATTCAT	TCTTCACCAC	AGACCCCAAC	TACACCCACC
7951	TCTGGAGCAA	ACTGGGAAAC	TTCAGCTACT	CCTGAGAGCC	TTTTGGTAGT
8001	CACTGAGACT	TCAGACACAA	CACTTACCTC	AAAGATTTTG	GTCACAGATA
8051	CCATCTTGTT	TTCAACTGTG	TCCACGCCAC	CTTCTAAATT	TCCAAGTACG
8101	GGGACTCTGT	CTGGAGCTTC	CTTCCCTACT	TTACTCCCGG	ACACTCCAGC
8151	CATCCCTCTC	ACTGCCACTG	AGCCAACAAG	TTCATTAGCT	ACATCCTTTG
8201	ATTCCACCCC	ACTGGTGACT	ATAGCTTCGG	ATAGTCTTGG	CACAGTCCCA
8251	GAGACTACCC	TGACCATGTC	AGAGACCTCA	AATGGTGATG	CACTGGTTCT
8301	TAAGACAGTA	AGTAACCCAG	ATAGGAGCAT	CCCTGGAATC	ACTATCCAAG
8351	GAGTAACAGA	AAGTCCACTC	CATCCTTCTT	CCACTTCCCC	CTCTAAGATT
8401	GTTGCTCCAC	GGAATACAAC	CTATGAAGGT	TCGATCACAG	TGGCACTTTC
8451	TACTTTGCCT	GCGGGAACTA	CTGGTTCCCT	TGTATTCACT	CAGAGTTCTG
8501	AAAACTCAGA	GACAACGGCT	TTGGTAGACT	CATCAGCTGG	GCTTGAGAGG
8551	GCATCTGTGA	TGCCACTAAC	CACAGGAAGC	CAGGGTATGG	CTAGCTCTGG
8601	AGGAATCAGA	AGTGGGTCCA	CTCACTCAAC	TGGAACCAAA	ACATTTTCTT
8651	CTCTCCCTCT	GACCATGAAC	CCAGGTGAGG	TTACAGCCAT	GTCTGAAATC
8701	ACCACGAACA	GACTGACAGC	TACTCAATCA	ACAGCACCCA	AAGGGATACC

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
8751	TGTGAAGCCC	ACCAGTGCTG	AGTCAGGCCT	CCTAACACCT	GTCTCTGCCT
8801	CCTCAAGCCC	ATCAAAGGCC	TTTGCCTCAC	TGACTACAGC	TCCCCCATCA
8851	ACTTGGGGGA	TCCCACAGTC	TACCTTGACA	TTTGAGTTTT	CTGAGGTCCC
8901	AAGTTTGGAT	ACTAAGTCCG	CTTCTTTACC	AACTCCTGGA	CAGTCCCTGA
8951	ACACCATTCC	AGACTCAGAT	GCAAGCACAG	CATCTTCCTC	ACTGTCCAAG
9001	TCTCCAGAAA	AAAACCCAAG	GGCAAGGATG	ATGACTTCCA	CAAAGGCCAT
9051	AAGTGCAAGC	TCATTTCAAT	CAACAGGTTT	TACTGAAACC	CCTGAGGGAT
9101	CTGCCTCCCC	TTCTATGGCA	GGGCATGAAC	CCAGAGTCCC	CAC TTCAGGA
9151	ACAGGGGACC	CTAGATATGC	CTCAGAGAGC	ATGTCTTATC	CAGACCCAAG
9201	CAAGGCATCA	TCAGCTATGA	CATCGACCTC	TCTTG CATCA	AAACTCACAA
9251	CTCTCTTCAG	CACAGGTCAA	GCAGCAAGGT	CTGGTTCTAG	TTCCTCTCCC
9301	ATAAGCCTAT	CCACTGAGAA	AGAAACAAGC	TTCCTTTCCC	CCACTGCATC
9351	CACCTCCAGA	AAGACTTCAC	TATTTCTTGG	GCCTTCCATG	GCAAGGCAGC
9401	CCAACATATT	GGTGCATCTT	CAGACTTCAG	CTCTGACACT	TTCTCCAACA
9451	TCCACTCTAA	ATATGTCCCA	GGAGGAGCCT	CCTGAGTTAA	CCTCAAGCCA
9501	GACCATTGCA	GAAGAAGAGG	GAACAACAGC	TGAAACACAG	ACGTTAACCT
9551	TCACACCATC	TGAGACCCCA	ACATCCTTGT	TACCTGTCTC	TTCTCCCACA
9601	GAACCCACAG	CCAGAAGAAA	GAGTTCTCCA	GAAACATGGG	CAAGCTCTAT
9651	TTCAGTTCCT	GCCAAGACCT	CCTTG GTTGA	AACAACTGAT	GGAACGCTAG
9701	TGACCACCAT	AAAGATGTCA	AGCCAGGCAG	CACAAGGAAA	TTCCACGTGG
9751	CCTGCCCCAG	CAGAGGAGAC	GGGGACCAGT	CCAGCAGGCA	CATCCCCAGG
9801	AAGCCCAGAA	GTGTCTACCA	CTCTCAAAAT	CATGAGCTCC	AAGGAACCCA
9851	GCATCAGCCC	AGAGATCAGG	TCCACTGTGC	GAAATTCTCC	TTGGAAGACT
9901	CCAGAAACAA	CTGTTCCCAT	GGAGACCACA	GTGGAACCAG	TCACCCTTCA
9951	GTCCACAGCC	CTAGGAAGTG	GCAGCACCAG	CATCTCTCAC	CTGCCCACAG



Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
10001	GAACCACATC	ACCAACCAAG	TCACCAACAG	AAAATATGTT	GGCTACAGAA
10051	AGGGTCTCCC	TCTCCCCATC	CCCACCTGAG	GCTTGGACCA	ACCTTTATTC
10101	TGGAActCCA	GGAGGGACCA	GGCAGTCACT	GGCCACAATG	TCCTCTGTCT
10151	CCCTAGAGTC	ACCAACTGCT	AGAAGCATCA	CAGGGACTGG	TCAGCAAAGC
10201	AGTCCAGAAC	TGGTTTCAAA	GACAACTGGA	ATGGAATTCT	CTATGTGGCA
10251	TGGCTCTACT	GGAGGGACCA	CAGGGGACAC	ACATGTCTCT	CTGAGCACAT
10301	CTTCCAATAT	CCTTGAAGAC	CCTGTAACCA	GCCCAAATC	TGTGAGCTCA
10351	TTGACAGATA	AATCCAAACA	TAAAACCGAG	ACATGGGTAA	GCACCACAGC
10401	CATTCCCTCC	ACTGTCCTGA	ATAATAAGAT	AATGGCAGCT	GAACAACAGA
10451	CAAGTCGATC	TGTGGATGAG	GCTTATTCAT	CAACTAGTTC	TTGGTCAGAT
10501	CAGACATCTG	GGAGTGACAT	CACCCTTGGT	GCATCTCCTG	ATGTCACAAA
10551	CACATTATAC	ATCACCTCCA	CAGCACAAAC	CACCTCACTA	GTGTCTCTGC
10601	CCTCTGGAGA	CCAAGGCATT	ACAAGCCTCA	CCAATCCCTC	AGGAGGAAAA
10651	ACAAGCTCTG	CGTCATCTGT	CACATCTCCT	TCAATAGGGC	TTGAGACTCT
10701	GAGGGCCAAT	GTAAGTGCAG	TGAAAAGTGA	CCTTGCCCT	ACTGCTGGGC
10751	ATCTATCTCA	GACTTCATCT	CCTGCGGAAG	TGAGCATCCT	GGACGTAACC
10801	ACAGCTCCTA	CTCCAGGTAT	CTCCACCACC	ATCACCACCA	TGGGAACCAA
10851	CTCAATCTCA	ACTACCACAC	CCAACCCAGA	AGTGGGTATG	AGTACCATGG
10901	ACAGCACCCC	GGCCACAGAG	AGGCGCACAA	CTTCTACAGA	ACACCCTTCC
10951	ACCTGGTCTT	CCACAGCTGC	ATCAGATTCC	TGGACTGTCA	CAGACATGAC
11001	TTCAAACCTG	AAAGTTGCAA	GATCTCCTGG	AACAATTTCC	ACAATGCATA
11051	CAACTTCATT	CTTAGCCTCA	AGCACTGAAT	TAGACTCCAT	GTCTACTCCC
11101	CATGGCCGTA	TAAGTGTGAT	TGGAACCAGC	CTGGTCACTC	CATCCTCTGA
11151	TGCTTCAGCT	GTAAAGACAG	AGACCAGTAC	AAGTGAAAGA	ACATTGAGTC
11201	CTTCAGACAC	AACTGCATCT	ACTCCCATCT	CAACTTTTTTC	TCGTGTCCAG

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
11251	AGGATGAGCA	TCTCAGTTCC	TGACATTTTA	AGTACAAGTT	GGACTCCCAG
11301	TAGTACAGAA	GCAGAAGATG	TGCCTGTTTC	AATGGTTTCT	ACAGATCATG
11351	CTAGTACAAA	GACTGACCCA	AATACGCCCC	TGTCCACTTT	TCTGTTTGAT
11401	TCTCTGTCCA	CTCTTGACTG	GGACACTGGG	AGATCTCTGT	CATCAGCCAC
11451	AGCCACTACC	TCAGCTCCTC	AGGGGGCCAC	AACTCCCCAG	GAACCTCACTT
11501	TGGAAACCAT	GATCAGCCCC	GCTACCTCAC	AGTTGCCCTT	CTCTATAGGG
11551	CACATTACAA	GTGCAGTCAC	ACCAGCTGCA	ATGGCAAGGA	GCTCTGGAGT
11601	TACTTTTTCA	AGACCAGATC	CCACAAGCAA	AAAGGCAGAG	CAGACTTCCA
11651	CTCAGCTTCC	CACCACCACT	TCTGCACATC	CAGGGCAGGT	GCCCAGATCA
11701	GCAGCAACAA	CTCTGGATGT	GATCCACAC	ACAGCAAAAA	CTCCAGATGC
11751	AACTTTTTCAG	AGACAAGGGC	AGACAGCTCT	TACAACAGAG	GCAAGAGCTA
11801	CATCTGACTC	CTGGAATGAG	AAAGAAAAAT	CAACCCCAAG	TGCACCTTGG
11851	ATCACTGAGA	TGATGAATTC	TGTCTCAGAA	GATACCATCA	AGGAGGTTAC
11901	CAGCTCCTCC	AGTGTATTAA	AGGACCCTGA	ATACGCTGGA	CATAAACTTG
11951	GAATCTGGGA	CGACTTCATC	CCAAGTTTG	GAAAAGCAGC	CCATATGAGA
12001	GAGTTGCCCC	TTCTGAGTCC	ACCACAGGAC	AAAGAGGCAA	TTCACCCCTTC
12051	TACAAACACA	GTAGAGACCA	CAGGCTGGGT	CACAAGTTCC	GAACATGCTT
12101	CTCATTCAC	TATCCCAGCC	CACTCAGCGT	CATCCAAACT	CACATCTCCA
12151	GTGGTTACAA	CCTCCACCAG	GGAACAAGCA	ATAGTTTCTA	TGTCAACAAC
12201	CACATGGCCA	GAGTCTACAA	GGGCTAGAAC	AGAGCCTAAT	TCCTTCTTGA
12251	CTATTGAACT	GAGGGACGTC	AGCCCTTACA	TGGACACCAG	CTCAACCACA
12301	CAAACAAGTA	TTATCTCTTC	CCCAGGTTCC	ACTGCGATCA	CCAAGGGGCC
12351	TAGAACAGAA	ATTACCTCCT	CTAAGAGAAT	ATCCAGCTCA	TTCCTTGCCC
12401	AGTCTATGAG	GTCGTCAGAC	AGCCCCTCAG	AAGCCATCAC	CAGGCTGTCT
12451	AACTTTCCTG	CCATGACAGA	ATCTGGAGGA	ATGATCCTTG	CTATGCAAAC

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**


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12501	AAGTCCACCT	GGCGCTACAT	CACTAAGTGC	ACCTACTTTG	GATACATCAG
12551	CCACAGCCTC	CTGGACAGGG	ACTCCACTGG	CTACGACTCA	GAGATTTACA
12601	TACTCAGAGA	AGACCACTCT	CTTTAGCAAA	GGTCCTGAGG	ATACATCACA
12651	GCCAAGCCCT	CCCTCTGTGG	AAGAAACCAG	CTCTTCCTCT	TCCCTGGTAC
12701	CTATCCATGC	TACAACCTCG	CCTTCCAATA	TTTTGTTGAC	ATCACAAGGG
12751	CACAGTCCCT	CCTCTACTCC	ACCTGTGACC	TCAGTTTTCT	TGTCTGAGAC
12801	CTCTGGCCTG	GGGAAGACCA	CAGACATGTC	GAGGATAAGC	TTGGAACCTG
12851	GCACAAGTTT	ACCTCCCAAT	TTGAGCAGTA	CAGCAGGTGA	GGCGTTATCC
12901	ACTTATGAAG	CCTCCAGAGA	TACAAAGGCA	ATTCATCATT	CTGCAGACAC
12951	AGCAGTGACG	AATATGGAGG	CAACCAGTTC	TGAATATTCT	CCTATCCCAG
13001	GCCATACAAA	GCCATCCAAA	GCCACATCTC	CATTGGTTAC	CTCCCACATC
13051	ATGGGGGACA	TCACTTCTTC	CACATCAGTA	TTTGGCTCCT	CCGAGACCAC
13101	AGAGATTGAG	ACAGTGTCTT	CTGTGAACCA	GGGACTTCAG	GAGAGAAGCA
13151	CATCCCAGGT	GGCCAGCTCT	GCTACAGAGA	CAAGCACTGT	CATTACCCAT
13201	GTGTCTAGTG	GTGATGCTAC	TACTCATGTC	ACCAAGACAC	AAGCCACTTT
13251	CTCTAGCGGA	ACATCCATCT	CAAGCCCTCA	TCAGTTTATA	ACTTCTACCA
13301	ACACATTTAC	AGATGTGAGC	ACCAACCCCT	CCACCTCTCT	GATAATGACA
13351	GAATCTTCAG	GAGTGACCAT	CACCACCCAA	ACAGGTCCTA	CTGGAGCTGC
13401	AACACAGGGT	CCATATCTCT	TGGACACATC	AACCATGCCT	TACTTGACAG
13451	AGACTCCATT	AGCTGTGACT	CCAGATTTTA	TGCAATCAGA	GAAGACCACT
13501	CTCATAAGCA	AAGGTCCCAA	GGATGTGACC	TGGACAAGCC	CTCCCTCTGT
13551	GGCAGAAACC	AGCTATCCCT	CTTCCCTGAC	ACCTTTCTTG	GTCACAACCA
13601	TACCTCCTGC	CACTTCCACG	TTACAAGGGC	AACATACATC	CTCTCCTGTT
13651	TCTGCGACTT	CAGTTCTTAC	CTCTGGACTG	GTGAAGACCA	CAGATATGTT
13701	GAACACAAGC	ATGGAACCTG	TGACCAATTC	ACCTCAAAAT	TTGAACAATC

Table 4 (continued)

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 Human cDNA of CA125  
 (SEQ ID NO: 4)
 

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13751	CATCAAATGA	GATACTGGCC	ACTTTGGCAG	CCACCACAGA	TATAGAGACT
13801	ATTCATCCTT	CCATAAACAA	AGCAGTGACC	AATATGGGGA	CTGCCAGTTC
13851	AGCACATGTA	CTGCATTCCA	CTCTCCCAGT	CAGCTCAGAA	CCATCTACAG
13901	CCACATCTCC	AATGGTTCCT	GCCTCCAGCA	TGGGGGACGC	TCTTGCTTCT
13951	ATATCAATAC	CTGGTTCTGA	GACCACAGAC	ATTGAGGGAG	AGCCAACATC
14001	CTCCCTGACT	GCTGGACGAA	AAGAGAACAG	CACCCTCCAG	GAGATGAACT
14051	CAACTACAGA	GTCAAACATC	ATCCTCTCCA	ATGTGTCTGT	GGGGGCTATT
14101	ACTGAAGCCA	CAAAAATGGA	AGTCCCCTCT	TTTGATGCAA	CATTCATACC
14151	AACTCCTGCT	CAGTCAACAA	AGTCCCAGAG	TATTTTCTCA	GTAGCCAGCA
14201	GTAGACTTTC	AAACTCTCCT	CCCATGACAA	TATCTACCCA	CATGACCACC
14251	ACCCAGACAG	GGTCTTCTGG	AGCTACATCA	AAGATTCCAC	TTGCCTTAGA
14301	CACATCAACC	TTGGAAACCT	CAGCAGGGAC	TCCATCAGTG	GTGACTGAGG
14351	GGTTTGCCCA	CTCAAAAATA	ACCACTGCAA	TGAACAATGA	TGTCAAGGAC
14401	GTGTCACAGA	CAAACCCTCC	CTTTCAGGAT	GAAGCCAGCT	CTCCCTCTTC
14451	TCAAGCACCT	GTCCTTGTC	CAACCTTACC	TTCTTCTGTT	GCTTTCACAC
14501	CGCAATGGCA	CAGTACCTCC	TCTCCTGTTT	CTATGTCCTC	AGTTCTTACT
14551	TCTTCACTGG	TAAAGACCGC	AGGCAAGGTG	GATACAAGCT	TAGAAACAGT
14601	GACCAGTTCA	CCTCAAAGTA	TGAGCAACAC	TTTGGATGAC	ATATCGGTCA
14651	CTTCAGCAGC	CACCACAGAT	ATAGAGACAA	CGCATCCTTC	CATAAACACA
14701	GTAGTTACCA	ATGTGGGGAC	CACCGGTTCA	GCATTTGAAT	CACATTCTAC
14751	TGTCTCAGCT	TACCCAGAGC	CATCTAAAGT	CACATCTCCA	AATGTTACCA
14801	CCTCCACCAT	GGAAGACACC	ACAATTTCCT	GATCAATACC	TAAATCCTCT
14851	AAGACTACAA	GAAGTACAGC	TGAGACAAC	TCCTCCCTGA	CTCCTAAACT
14901	GAGGGAGACC	AGCATCTCCC	AGGAGATCAC	CTCGTCCACA	GAGACAAGCA
14951	CTGTTCCCTTA	CAAAGAGCTC	ACTGGTGCCA	CTACCGAGGT	ATCCAGGACA

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
15001	GATGTCACTT	CCTCTAGCAG	TACATCCTTC	CCTGGCCCTG	ATCAGTCCAC
15051	AGTGTCACTA	GACATCTCCA	CAGAAACCAA	CACCAGGCTG	TCTACCTCCC
15101	CAATAATGAC	AGAATCTGCA	GAAATAACCA	TCACCACCCA	AACAGGTCCT
15151	CATGGGGCTA	CATCACAGGA	TACTTTTACC	ATGGACCCAT	CAAATACAAC
15201	CCCCCAGGCA	GGGATCCACT	CAGCTATGAC	TCATGGATTT	TCACAATTGG
15251	ATGTGACCAC	TCTTATGAGC	AGAATTCCAC	AGGATGTATC	ATGGACAAGT
15301	CCTCCCTCTG	TGGATAAAAC	CAGCTCCCCC	TCTTCCTTTC	TGTCCTCACC
15351	TGCAATGACC	ACACCTTCCC	TGATTTCTTC	TACCTTACCA	GAGGATAAGC
15401	TCTCCTCTCC	TATGACTTCA	CTTCTCACCT	CTGGCCTAGT	GAAGATTACA
15451	GACATATTAC	GTACACGCTT	GGAACCTGTG	ACCAGCTCAC	TTCCAAATTT
15501	CAGCAGCACC	TCAGATAAGA	TACTGGCCAC	TTCTAAAGAC	AGTAAAGACA
15551	CAAAGGAAAT	TTTTCTTCT	ATAACACAG	AAGAGACCAA	TGTGAAAGCC
15601	AACAACCTCTG	GACATGAATC	CCATTCCCCT	GCACTGGCTG	ACTCAGAGAC
15651	ACCCAAAGCC	ACAAC TCAA	TGGTTATCAC	CACCACTGTG	GGAGATCCAG
15701	CTCCTTCCAC	ATCAATGCCA	GTGCATGGTT	CCTCTGAGAC	TACAAACATT
15751	AAGAGAGAGC	CAACATATTT	CTTGACTCCT	AGACTGAGAG	AGACCAGTAC
15801	CTCTCAGGAG	TCCAGCTTTC	CCACGGACAC	AAGTTTCTA	CTTTCCAAAG
15851	TCCCCACTGG	TACTATTACT	GAGGTCTCCA	GTACAGGGGT	CAACTCTTCT
15901	AGCAAAATTT	CCACCCCAGA	CCATGATAAG	TCCACAGTGC	CACCTGACAC
15951	CTTCACAGGA	GAGATCCCCA	GGGTCTTCAC	CTCCTCTATT	AAGACAAAAT
16001	CTGCAGAAAT	GACGATCACC	ACCCAAGCAA	GTCCTCCTGA	GTCTGCATCG
16051	CACAGTACCC	TTCCCTTGGA	CACATCAACC	ACACTTTCCC	AGGGAGGGAC
16101	TCATTCAACT	GTGACTCAGG	GATTCCCAT	CTCAGAGGTG	ACCACTCTCA
16151	TGGGCATGGG	TCCTGGGAAT	GTGTCATGGA	TGACAACTCC	CCCTGTGGAA
16201	GAAACCAGCT	CTGTGTCTTC	CCTGATGTCT	TCACCTGCCA	TGACATCCCC

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
16251	TTCTCCTGTT	TCCTCCACAT	CACCACAGAG	CATCCCCTCC	TCTCCTCTTC
16301	CTGTGACTGC	ACTTCCTACT	TCTGTTCTGG	TGACAACCAC	AGATGTGTTG
16351	GGCACAACAA	GCCCAGAGTC	TGTAACCAGT	TCACCTCCAA	ATTGAGCAG
16401	CATCACTCAT	GAGAGACCGG	CCACTTACAA	AGACACTGCA	CACACAGAAG
16451	CCGCCATGCA	TCATTCCACA	AACACCGCAG	TGACCAATGT	AGGGACTTCC
16501	GGGTCTGGAC	ATAAATCACA	ATCCTCTGTC	CTAGCTGACT	CAGAGACATC
16551	GAAAGCCACA	CCTCTGATGA	GTACCACCTC	CACCCTGGGG	GACACAAGTG
16601	TTTCCACATC	AACTCCTAAT	ATCTCTCAGA	CTAACCAAAT	TCAAACAGAG
16651	CCAACAGCAT	CCCTGAGCCC	TAGACTGAGG	GAGAGCAGCA	CGTCTGAGAA
16701	GACCAGCTCA	ACAACAGAGA	CAAATACTGC	CTTTTCTTAT	GTGCCACAG
16751	GTGCTATTAC	TCAGGCCTCC	AGAACAGAAA	TCTCCTCTAG	CAGAACATCC
16801	ATCTCAGACC	TTGATCGGCC	CACAATAGCA	CCCGACATCT	CCACAGGAAT
16851	GATCACCAGG	CTCTTCACCT	CCCCCATCAT	GACAAAATCT	GCAGAAATGA
16901	CCGTCACCAC	TCAAACAAC	ACTCCTGGGG	CTACATCACA	GGGTATCCTT
16951	CCTTGGGACA	CATCAACCAC	ACTTTTCCAG	GGAGGGACTC	ATTCAACCGT
17001	GTCTCAGGGA	TTCCCACACT	CAGAGATAAC	CACTCTTCGG	AGCAGAACCC
17051	CTGGAGATGT	GTCATGGATG	ACAACTCCCC	CTGTGGAAGA	AACCAGCTCT
17101	GGGTTTCCC	TGATGTCACC	TTCCATGACA	TCCCCTTCTC	CTGTTTCCTC
17151	CACATCACCA	GAGAGCATCC	CCTCCTCTCC	TCTCCCTGTG	ACTGCACTTC
17201	TTACTTCTGT	TCTGGTGACA	ACCACCAATG	TATTGGGCAC	AACAAGCCCA
17251	GAGACCGTAA	CGAGTTCACC	TCCAAATTTA	AGCAGCCCCA	CACAGGAGAG
17301	ACTGACCACT	TACAAAGACA	CTGCGCACAC	AGAAGCCATG	CATGCTTCCA
17351	TGCATACAAA	CACTGCAGTG	GCCAACGTCG	GGACCTCCAT	TTCTGGACAT
17401	GAATCACAAT	CTTCTGTCCC	AGCTGATTCA	CACACATCCA	AAGCCACATC
17451	TCCAATGGGT	ATCACCTTCG	CCATGGGGGA	TACAAGTGTT	TCTACATCAA

Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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17501	CTCCTGCCTT	CTTTGAGACT	AGAATTCAGA	CTGAATCAAC	ATCCTCTTTG
17551	ATTCTTGGAT	TAAGGGACAC	CAGGACGTCT	GAGGAGATCA	ACACTGTGAC
17601	AGAGACCAGC	ACTGTCCTTT	CAGAAGTGCC	CACTACTACT	ACTACTGAGG
17651	TCTCCAGGAC	AGAAGTTATC	ACTTCCAGCA	GAACAACCAT	CTCAGGGCCT
17701	GATCATTTCCA	AAATGTCACC	CTACATCTCC	ACAGAAACCA	TCACCAGGCT
17751	CTCCACTTTT	CCTTTTGTA	CAGGATCCAC	AGAAATGGCC	ATCACCAACC
17801	AAACAGGTCC	TATAGGGACT	ATCTCACAGG	CTACCCTTAC	CCTGGACACA
17851	TCAAGCACAG	CTTCCTGGGA	AGGGACTCAC	TCACCTGTGA	CTCAGAGATT
17901	TCCACACTCA	GAGGAGACCA	CTACTATGAG	CAGAAGTACT	AAGGGCGTGT
17951	CATGGCAAAG	CCCTCCCTCT	GTGGAAGAAA	CCAGTTCTCC	TTCTTCCCCA
18001	GTGCCTTTAC	CTGCAATAAC	CTCACATTCA	TCTCTTTATT	CCGCAGTATC
18051	AGGAAGTAGC	CCCATTCTG	CTCTCCCTGT	GACTTCCCTT	CTCACCTCTG
18101	GCAGGAGGAA	GACCATAGAC	ATGTTGGACA	CACACTCAGA	ACTTGTGACC
18151	AGCTCCTTAC	CAAGTGCAAG	TAGCTTCTCA	GGTGAGATAC	TCATTCTGA
18201	AGCCTCCACA	AATACAGAGA	CAATTCACCT	TTCAGAGAAC	ACAGCAGAAA
18251	CCAATATGGG	GACCACCAAT	TCTATGCATA	AACTACATTC	CTCTGTCTCA
18301	ATCCACTCCC	AGCCATCCGG	ACACACACCT	CAAAGGTTA	CTGGATCTAT
18351	GATGGAGGAC	GCTATTGTTT	CCACATCAAC	ACCTGGTTCT	CCTGAGACTA
18401	AAAATGTTGA	CAGAGACTCA	ACATCCCCTC	TGACTCCTGA	ACTGAAAGAG
18451	GACAGCACCG	CCCTGGTGAT	GAACTCAACT	ACAGAGTCAA	ACACTGTTTT
18501	CTCCAGTGTG	TCCCTGGATG	CTGCTACTGA	GGTCTCCAGG	GCAGAAGTCA
18551	CCTACTATGA	TCCTACATTC	ATGCCAGCTT	CTGCTCAGTC	AACAAAGTCC
18601	CCAGACATTT	CACCTGAAGC	CAGCAGCAGT	CATTCTAACT	CTCCTCCCTT
18651	GACAATATCT	ACACACAAGA	CCATCGCCAC	ACAAACAGGT	CCTTCTGGGG
18701	TGACATCTCT	TGGCCAACTG	ACCCTGGACA	CATCAACCAT	AGCCACCTCA

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
18751	GCAGGAACTC	CATCAGCCAG	AACTCAGGAT	TTTGTAGATT	CAGAAACAAC
18801	CAGTGTCATG	AACAATGATC	TCAATGATGT	GTTGAAGACA	AGCCCTTTCT
18851	CTGCAGAAGA	AGCCAACTCT	CTCTCTTCTC	AGGCACCTCT	CCTTGTGACA
18901	ACCTCACCTT	CTCCTGTAAC	TTCCACATTG	CAAGAGCACA	GTACCTCCTC
18951	TCTTGTTTCT	GTGACCTCAG	TACCCACCCC	TACACTGGCG	AAGATCACAG
19001	ACATGGACAC	AAACTTAGAA	CCTGTGACTC	GTTACCTCA	AAATTTAAGG
19051	AACACCTTGG	CCACTTCAGA	AGCCACCACA	GATACACACA	CAATGCATCC
19101	TTCTATAAAC	ACAGCAATGG	CCAATGTGGG	GACCACCAGT	TCACCAAATG
19151	AATTCTATTT	TACTGTCTCA	CCTGACTCAG	ACCCATATAA	AGCCACATCC
19201	GCAGTAGTTA	TCACTTCCAC	CTCGGGGGAC	TCAATAGTTT	CCACATCAAT
19251	GCCTAGATCC	TCTGCGATGA	AAAAGATTGA	GTCTGAGACA	ACTTTCTCCC
19301	TGATATTTAG	ACTGAGGGAG	ACTAGCACCT	CCCAGAAAAT	TGGCTCATCC
19351	TCAGACACAA	GCACGGTCTT	TGACAAAGCA	TTCCTGCTG	CTACTACTGA
19401	GGTCTCCAGA	ACAGAACTCA	CCTCCTCTAG	CAGAACATCC	ATCCAAGGCA
19451	CTGAAAAGCC	CACAATGTCA	CCGGACACCT	CCACAAGATC	TGTCACCATG
19501	CTTTCTACTT	TTGCTGGCCT	GACAAAATCC	GAAGAAAGGA	CCATTGCCAC
19551	CCAAACAGGT	CCTCATAGGG	CGACATCACA	GGGTACCCTT	ACCTGGGACA
19601	CATCAATCAC	AACCTCACAG	GCAGGGACCC	ACTCAGCTAT	GACTCATGGA
19651	TTTTTACAAT	TAGATTTGTC	CACTCTTACG	AGTAGAGTTC	CTGAGTACAT
19701	ATCAGGGACA	AGCCCACCCT	CTGTGGAAAA	AACCAGCTCT	TCCTCTTCCC
19751	TTCTGTCTTT	ACCAGCAATA	ACCTCACCGT	CCCCTGTACC	TACTACATTA
19801	CCAGAAAGTA	GGCCGTCTTC	TCCTGTTTCAT	CTGACTTCAC	TCCCCACCTC
19851	TGGCCTAGTG	AAGACCACAG	ATATGCTGGC	ATCTGTGGCC	AGTTTACCTC
19901	CAAACCTGGG	CAGCACCTCA	CATAAGATAC	CGACTACTTC	AGAAGACATT
19951	AAAGATACAG	AGAAAATGTA	TCCTTCCACA	AACATAGCAG	TAACCAATGT



Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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20001	GGGGACCACC	ACTTCTGAAA	AGGAATCTTA	TTCGTCTGTC	CCAGCCTACT
20051	CAGAACCACC	CAAAGTCACC	TCTCCAATGG	TTACCTCTTT	CAACATAAGG
20101	GACACCATTG	TTCCACATC	CATGCCTGGC	TCCTCTGAGA	TTACAAGGAT
20151	TGAGATGGAG	TCAACATTCT	CCGTGGCTCA	TGGGCTGAAG	GGAACCAGCA
20201	CCTCCCAGGA	CCCCATCGTA	TCCACAGAGA	AAAGTGCTGT	CCTTCACAAG
20251	TTGACCACTG	GTGCTACTGA	GACCTCTAGG	ACAGAAGTTG	CCTCTTCTAG
20301	AAGAACATCC	ATTCCAGGCC	CTGATCATTC	CACAGAGTCA	CCAGACATCT
20351	CCACTGAAGT	GATCCCCAGC	CTGCCTATCT	CCCTTGGCAT	TACAGAATCT
20401	TCAAATATGA	CCATCATCAC	TCGAACAGGT	CCTCCTCTTG	GCTCTACATC
20451	ACAGGGCACA	TTTACCTTGG	ACACACCAAC	TACATCCTCC	AGGGCAGGAA
20501	CACACTCGAT	GGCGACTCAG	GAATTTCCAC	ACTCAGAAAT	GACCACTGTC
20551	ATGAACAAGG	ACCCTGAGAT	TCTATCATGG	ACAATCCCTC	CTTCTATAGA
20601	GAAAACCAGC	TTCTCCTCTT	CCCTGATGCC	TTCACCAGCC	ATGACTTCAC
20651	CTCCTGTTTC	CTCAACATTA	CCAAAGACCA	TTACACCCAC	TCCTTCTCCT
20701	ATGACCTCAC	TGCTCACCCC	TAGCCTAGTG	ATGACCACAG	ACACATTGGG
20751	CACAAGCCCA	GAACCTACAA	CCAGTTCACC	TCCAAATTTG	AGCAGTACCT
20801	CACATGTGAT	ACTGACAACA	GATGAAGACA	CCACAGCTAT	AGAAGCCATG
20851	CATCCTTCCA	CAAGCACAGC	AGCGACTAAT	GTGGAAACCA	CCTGTTCTGG
20901	ACATGGGTCA	CAATCCTCTG	TCCTAACTGA	CTCAGAAAAA	ACCAAGGCCA
20951	CAGCTCCAAT	GGATACCACC	TCCACCATGG	GGCATACAAC	TGTTTCCACA
21001	TCAATGTCTG	TTTCCTCTGA	GACTACAAAA	ATTAAGAGAG	AGTCAACATA
21051	TTCTTGA	CCTGGACTGA	GAGAGACCAG	CATTTCCCAA	AATGCCAGCT
21101	TTTCCACTGA	CACAAGTATT	GTTCTTTCAG	AAGTCCCCAC	TGGTACTACT
21151	GCTGAGGTCT	CCAGGACAGA	AGTCACCTCC	TCTGGTAGAA	CATCCATCCC
21201	TGGCCCTTCT	CAGTCCACAG	TTTTGCCAGA	AATATCCACA	AGAACAATGA

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Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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21251	CAAGGCTCTT	TGCCTCGCCC	ACCATGACAG	AATCAGCAGA	AATGACCATC
21301	CCCACTCAAA	CAGGTCCTTC	TGGGTCTACC	TCACAGGATA	CCCTTACCTT
21351	GGACACATCC	ACCACAAAGT	CCCAGGCAAA	GACTCATTCA	ACTTTGACTC
21401	AGAGATTTCC	ACACTCAGAG	ATGACCACTC	TCATGAGCAG	AGGTCTTGGA
21451	GATATGTCAT	GGCAAAGCTC	TCCCTCTCTG	GAAAATCCCA	GCTCTCTCCC
21501	TTCCCTGCTG	TCTTTACCTG	CCACAACCTC	ACCTCCTCCC	ATTTCTCCA
21551	CATTACCAGT	GACTATCTCC	TCCTCTCCTC	TTCTGTGAC	TTCACTTCTC
21601	ACCTCTAGCC	CGGTAACGAC	CACAGACATG	TTACACACAA	GCCCAGAACT
21651	TGTAACCAGT	TCACCTCCAA	AGCTGAGCCA	CAC TTCAGAT	GAGAGACTGA
21701	CCACTGGCAA	GGACACCACA	AATACAGAAG	CTGTGCATCC	TTCCACAAAC
21751	ACAGCAGCGT	CCAATGTGGA	GATTCCCAGC	TTTGGACATG	AATCCCCTTC
21801	CTCTGCCTTA	GCTGACTCAG	AGACATCCAA	AGCCACATCA	CCAATGTTTA
21851	TTACCTCCAC	CCAGGAGGAT	ACAACTGTTG	CCATATCAAC	CCCTCACTTC
21901	TTGGAGACTA	GCAGAATTCA	GAAAGAGTCA	ATTCCTCCC	TGAGCCCTAA
21951	ATTGAGGGAG	ACAGGCAGTT	CTGTGGAGAC	AAGCTCAGCC	ATAGAGACAA
22001	GTGCTGTCCT	TTCTGAAGTG	TCCATTGGTG	CTACTACTGA	GATCTCCAGG
22051	ACAGAAGTCA	CCTCCTCTAG	CAGAACATCC	ATCTCTGGTT	CTGCTGAGTC
22101	CACAATGTTG	CCAGAAATAT	CCACCACAAG	AAAAATCATT	AAGTTCCCTA
22151	CTTCCCCCAT	CCTGGCAGAA	TCATCAGAAA	TGACCATCAA	GACCCAAACA
22201	AGTCCTCCTG	GGTCTACATC	AGAGAGTACC	TTTACATTAG	ACACATCAAC
22251	CACTCCCTCC	TTGGTAATAA	CCCATTCGAC	TATGACTCAG	AGATTGCCAC
22301	ACTCAGAGAT	AACCACTCTT	GTGAGTAGAG	GTGCTGGGGA	TGTGCCACGG
22351	CCCAGCTCTC	TCCCTGTGGA	AGAAACAAGC	CCTCCATCTT	CCCAGCTGTC
22401	TTTATCTGCC	ATGATCTCAC	CTTCTCCTGT	TTCTTCCACA	TTACCAGCAA
22451	GTAGCCACTC	CTCTTCTGCT	TCTGTGACTT	CACCTCTCAC	ACCAGGCCAA

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Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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22501	GTGAAGACTA	CTGAGGTGTT	GGACGCAAGT	GCAGAACCTG	AAACCAGTTC
22551	ACCTCCAAGT	TTGAGCAGCA	CCTCAGTTGA	AATACTGGCC	ACCTCTGAAG
22601	TCACCACAGA	TACGGAGAAA	ATTCATCCTT	TCCCAAACAC	GGCAGTAACC
22651	AAAGTTGGAA	CTTCCAGTTC	TGGACATGAA	TCCCCTTCCT	CTGTCCTACC
22701	TGACTCAGAG	ACAACCAAAG	CCACATCGGC	AATGGGTACC	ATCTCCATTA
22751	TGGGGGATAC	AAGTGTTTCT	ACATTAACTC	CTGCCTTATC	TAACACTAGG
22801	AAAATTTCAGT	CAGAGCCAGC	TTCCTCACTG	ACCACCAGAT	TGAGGGAGAC
22851	CAGCACCTCT	GAAGAGACCA	GCTTAGCCAC	AGAAGCAAAC	ACTGTTCTTT
22901	CTAAAGTGTC	CACTGGTGCT	ACTACTGAGG	TCTCCAGGAC	AGAAGCCATC
22951	TCCTTTAGCA	GAACATCCAT	GTCAGGCCCT	GAGCAGTCCA	CAATGTCACA
23001	AGACATCTCC	ATAGGAACCA	TCCCCAGGAT	TTCTGCCTCC	TCTGTCTCTGA
23051	CAGAATCTGC	AAAAATGACC	ATCACAACCC	AAACAGGTCC	TTCGGAGTCT
23101	ACACTAGAAA	GTACCCCTTAA	TTTGAACACA	GCAACCACAC	CCTCTTGGGT
23151	GGAAACCCAC	TCTATAGTAA	TTCAGGGATT	TCCACACCCA	GAGATGACCA
23201	CTTCCATGGG	CAGAGGTCCT	GGAGGTGTGT	CATGGCCTAG	CCCTCCCTTT
23251	GTGAAAGAAA	CCAGCCCTCC	ATCCTCCCCG	CTGTCTTTAC	CTGCCGTGAC
23301	CTCACCTCAT	CCTGTTTCCA	CCACATTCTT	AGCACATATC	CCCCCTCTC
23351	CCCTTCCTGT	GACTTCACTT	CTCACCTCTG	GCCCGGCGAC	AACCACAGAT
23401	ATCTTGGGTA	CAAGCACAGA	ACCTGGAACC	AGTTCATCTT	CAAGTTTGAG
23451	CACCACCTCC	CATGAGAGAC	TGACCACTTA	CAAAGACACT	GCACATACAG
23501	AAGCCGTGCA	TCCTTCCACA	AACACAGGAG	GGACCAATGT	GGCAACCACC
23551	AGCTCTGGAT	ATAAATCACA	GTCCTCTGTC	CTAGCTGACT	CATCTCCAAT
23601	GTGTACCACC	TCCACCATGG	GGGATACAAG	TGTTCTCACA	TCAACTCCTG
23651	CCTTCCTTGA	GACTAGGAGG	ATTCAGACAG	AGCTAGCTTC	CTCCCTGACC
23701	CCTGGATTGA	GGGAGTCCAG	TGGCTCTGAA	GGGACCAGCT	CAGGCACCAA

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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23751	GATGAGCACT	GTCCTCTCTA	AAGTGCCAC	TGGTGCTACT	ACTGAGATCT
23801	CCAAGGAAGA	CGTCACCTCC	ATCCCAGGTC	CCGCTCAATC	CACAATATCA
23851	CCAGACATCT	CCACAAGAAC	CGTCAGCTGG	TTCTCTACAT	CCCCTGTCAT
23901	GACAGAATCA	GCAGAAATAA	CCATGAACAC	CCATACAAGT	CCTTTAGGGG
23951	CCACAACACA	AGGCACCAGT	ACTTTGGCCA	CGTCAAGCAC	AACCTCTTTG
24001	ACAATGACAC	ACTCAACTAT	ATCTCAAGGA	TTTTCACACT	CACAGATGAG
24051	CACTCTTATG	AGGAGGGGTC	CTGAGGATGT	ATCATGGATG	AGCCCTCCCC
24101	TTCTGGAAAA	AACTAGACCT	TCCTTTTCTC	TGATGTCTTC	ACCAGCCACA
24151	ACTTCACCTT	CTCCTGTTTC	CTCCACATTA	CCAGAGAGCA	TCTCTTCCTC
24201	TCCTCTTCCT	GTGACTTCAC	TCCTCACGTC	TGGCTTGGCA	AAACTACAG
24251	ATATGTTGCA	CAAAAGCTCA	GAACCTGTAA	CCAACTCACC	TGCAAATTTG
24301	AGCAGCACCT	CAGTTGAAAT	ACTGGCCACC	TCTGAAGTCA	CCACAGATAC
24351	AGAGAAAAC	CATCCTTCTT	CAACAGAAC	AGTGACCGAT	GTGGGGACCT
24401	CCAGTTCTGG	ACATGAATCC	ACTTCCTTTG	TCCTAGCTGA	CTCACAGACA
24451	TCCAAAGTCA	CATCTCCAAT	GGTTATTACC	TCCACCATGG	AGGATACGAG
24501	TGTCTCCACA	TCAACTCCTG	GCTTTTTTGA	GACTAGCAGA	ATTCAGACAG
24551	AACCAACATC	CTCCCTGACC	CTTGGACTGA	GAAAGACCAG	CAGCTCTGAG
24601	GGGACCAGCT	TAGCCACAGA	GATGAGCACT	GTCCTTTCTG	GAGTGCCAC
24651	TGGTGCCACT	GCTGAAGTCT	CCAGGACAGA	AGTCACCTCC	TCTAGCAGAA
24701	CATCCATCTC	AGGCTTTGCT	CAGCTCACAG	TGTCACCAGA	GACTTCCACA
24751	GAAACCATCA	CCAGACTCCC	TACCTCCAGC	ATAATGACAG	AATCAGCAGA
24801	AATGATGATC	AAGACACAAA	CAGATCCTCC	TGGGTCTACA	CCAGAGAGTA
24851	CTCATACTGT	GGACATATCA	ACAACACCCA	ACTGGGTAGA	AACCCACTCG
24901	ACTGTGACTC	AGAGATTTTC	AACTCAGAG	ATGACCACTC	TTGTGAGCAG
24951	AAGCCCTGGT	GATATGTTAT	GGCCTAGTCA	ATCCTCTGTG	GAAGAAACCA

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Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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25001	GCTCTGCCTC	TCCCTGCTG	TCTCTGCCTG	CCACGACCTC	ACCTTCTCCT
25051	GTTTCCTCTA	CATTAGTAGA	GGATTTCCCT	TCCGCTTCTC	TTCCTGTGAC
25101	TTCTCTTCTC	ACCCCTGGCC	TGGTGATAAC	CACAGACAGG	ATGGGCATAA
25151	GCAGAGAACC	TGGAACCAGT	TCCACTTCAA	ATTTGAGCAG	CACCTCCCAT
25201	GAGAGACTGA	CCACTTTGGA	AGACACTGTA	GATACAGAAG	ACATGCAGCC
25251	TTCCACACAC	ACAGCAGTGA	CCAACGTGAG	GACCTCCATT	TCTGGACATG
25301	AATCACAATC	TTCTGTCCTA	TCTGACTCAG	AGACACCCAA	AGCCACATCT
25351	CCAATGGGTA	CCACCTACAC	CATGGGGGAA	ACGAGTGTTT	CCATATCCAC
25401	TTCTGACTTC	TTTGAGACCA	GCAGAATTCA	GATAGAACCA	ACATCCTCCC
25451	TGACTTCTGG	ATTGAGGGAG	ACCAGCAGCT	CTGAGAGGAT	CAGCTCAGCC
25501	ACAGAGGGAA	GCACTGTCCT	TTCTGAAGTG	CCCAGTGGTG	CTACCACTGA
25551	GGTCTCCAGG	ACAGAAGTGA	TATCCTCTAG	GGGAACATCC	ATGTCAGGGC
25601	CTGATCAGTT	CACCATATCA	CCAGACATCT	CTACTGAAGC	GATCACCAGG
25651	CTTTCTACTT	CCCCATTAT	GACAGAATCA	GCAGAAAGTG	CCATCACTAT
25701	TGAGACAGGT	TCTCCTGGGG	CTACATCAGA	GGGTACCCTC	ACCTTGGACA
25751	CCTCAACAAC	AACCTTTTGG	TCAGGGACCC	ACTCAACTGC	ATCTCCAGGA
25801	TTTTCACACT	CAGAGATGAC	CACTCTTATG	AGTAGAACTC	CTGGAGATGT
25851	GCCATGGCCG	AGCCTTCCCT	CTGTGGAAGA	AGCCAGCTCT	GTCTCTTCCT
25901	CACTGTCTTC	ACCTGCCATG	ACCTCAACTT	CTTTTTTCTC	CGCATTACCA
25951	GAGAGCATCT	CCTCCTCTCC	TCATCCTGTG	ACTGCACTTC	TCACCCTTGG
26001	CCCAGTGAAG	ACCACAGACA	TGTTGCGCAC	AAGCTCAGAA	CCTGAAACCA
26051	GTTACCTCC	AAATTTGAGC	AGCACCTCAG	CTGAAATATT	AGCCACGTCT
26101	GAAGTCACCA	AAGATAGAGA	GAAAATTCAT	CCCTCCTCAA	ACACACCTGT
26151	AGTCAATGTA	GGGACTGTGA	TTTATAAACA	TCTATCCCCT	TCCTCTGTTT
26201	TGGCTGACTT	AGTGACAACA	AAACCCACAT	CTCCAATGGC	TACCACCTCC

Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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26251	ACTCTGGGGA	ATACAAGTGT	TTCCACATCA	ACTCCTGCCT	TCCCAGAAAC
26301	TATGATGACA	CAGCCAACTT	CCTCCCTGAC	TTCTGGATTA	AGGGAGATCA
26351	GTACCTCTCA	AGAGACCAGC	TCAGCAACAG	AGAGAAGTGC	TTCTCTTTCT
26401	GGAATGCCCA	CTGGTGCTAC	TACTAAGGTC	TCCAGAACAG	AAGCCCTCTC
26451	CTTAGGCAGA	ACATCCACCC	CAGGTCCTGC	TCAATCCACA	ATATCACCAG
26501	AAATCTCCAC	GGAAACCATC	ACTAGAATTT	CTACTCCCCT	CACCACGACA
26551	GGATCAGCAG	AAATGACCAT	CACCCCCAAA	ACAGGTCATT	CTGGGGCATC
26601	CTCACAAGGT	ACCTTTACCT	TGGACACATC	AAGCAGAGCC	TCCTGGCCAG
26651	GAACTCACTC	AGCTGCAACT	CACAGATCTC	CACACTCAGG	GATGACCACT
26701	CCTATGAGCA	GAGGTCCTGA	GGATGTGTCA	TGGCCAAGCC	GCCCATCAGT
26751	GGAAAAAACT	AGCCCTCCAT	CTTCCCTGGT	GTCTTTATCT	GCAGTAACCT
26801	CACCTTCGCC	ACTTTATTCC	ACACCATCTG	AGAGTAGCCA	CTCATCTCCT
26851	CTCCGGGTGA	CTTCTCTTTT	CACCCCTGTC	ATGATGAAGA	CCACAGACAT
26901	GTTGGACACA	AGCTTGGAAC	CTGTGACCAC	TTACCTCCC	AGTATGAATA
26951	TCACCTCAGA	TGAGAGTCTG	GCCACTTCTA	AAGCCACCAT	GGAGACAGAG
27001	GCAATTCAGC	TTTCAGAAAA	CACAGCTGTG	ACTCAGATGG	GCACCATCAG
27051	CGCTAGACAA	GAATTCTATT	CCTCTTATCC	AGGCCTCCCA	GAGCCATCCA
27101	AAGTGACATC	TCCAGTGGTC	ACCTCTTCCA	CCATAAAAGA	CATTGTTTCT
27151	ACAACCATAC	CTGCTTCCTC	TGAGATAACA	AGAATTGAGA	TGGAGTCAAC
27201	ATCCACCCTG	ACCCCCACAC	CAAGGGAGAC	CAGCACCTCC	CAGGAGATCC
27251	ACTCAGCCAC	AAAGCCAAGC	ACTGTTTCCTT	ACAAGGCACT	CACTAGTGCC
27301	ACGATTGAGG	ACTCCATGAC	ACAAGTCATG	TCCTCTAGCA	GAGGACCTAG
27351	CCCTGATCAG	TCCACAATGT	CACAAGACAT	ATCCAGTGAA	GTGATCACCA
27401	GGCTCTCTAC	CTCCCCCATC	AAGGCAGAAT	CTACAGAAAT	GACCATTACC
27451	ACCCAAACAG	GTTCTCCTGG	GGCTACATCA	AGGGGTACCC	TTACCTTGGA

Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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27501  CACTTCAACA ACTTTTATGT CAGGGACCCA CTCAACTGCA TCTCAAGGAT
27551  TTTCACACTC ACAGATGACC GCTCTTATGA GTAGAACTCC TGGAGATGTG
27601  CCATGGCTAA GCCATCCCTC TGTGGAAGAA GCCAGCTCTG CCTCTTTCTC
27651  ACTGTCTTCA CCTGTCATGA CCTCATCTTC TCCCGTTTCT TCCACATTAC
27701  CAGACAGCAT CCACTCTTCT TCGCTTCCTG TGACATCACT TCTCACCTCA
27751  GGGCTGGTGA AGACCACAGA GCTGTTGGGC ACAAGCTCAG AACCTGAAAC
27801  CAGTTCACCC CCAAATTTGA GCAGCACCTC AGCTGAAATA CTGGCCACCA
27851  CTGAAGTCAC TACAGATACA GAGAACTGG AGATGACCAA TGTGGTAACC
27901  TCAGGTTATA CACATGAATC TCCTTCCTCT GTCCTAGCTG ACTCAGTGAC
27951  AACAAAGGCC ACATCTTCAA TGGGTATCAC CTACCCACCA GGAGATACAA
28001  ATGTTCTCAC ATCAACCCCT GCCTTCTCTG ACACCAGTAG GATTCAAACA
28051  AAGTCAAAGC TCTCACTGAC TCCTGGGTTG ATGGAGACCA GCATCTCTGA
28101  AGAGACCAGC TCTGCCACAG AAAAAAGCAC TGTCTTTCT AGTGTGCCCCA
28151  CTGGTGCTAC TACTGAGGTC TCCAGGACAG AAGCCATCTC TTCTAGCAGA
28201  ACATCCATCC CAGGCCCTGC TCAATCCACA ATGTCATCAG ACACCTCCAT
28251  GGAAACCATC ACTAGAATTT CTACCCCCT CACAAGGAAA GAATCAACAG
28301  ACATGGCCAT CACCCCCAAA ACAGGTCCTT CTGGGGCTAC CTCGCAGGGT
28351  ACCTTTACCT TGGACTCATC AAGCACAGCC TCCTGGCCAG GAACTCACTC
28401  AGCTACAACT CAGAGATTTC CACAGTCAGT GGTGACAACT CCTATGAGCA
28451  GAGGTCTCTG GGATGTGTCA TGGCCAAGCC CGCTGTCTGT GGAAAAAACC
28501  AGCCCTCCAT CTTCCCTGGT ATCTTCATCT TCAGTAACCT CACCTTCGCC
28551  ACTTTATTCC ACACCATCTG GGAGTAGCCA CTCCTCTCCT GTCCCTGTCA
28601  CTTCTCTTTT CACCTCTATC ATGATGAAGG CCACAGACAT GTTGGATGCA
28651  AGTTTGGAAC CTGAGACCAC TTCAGCTCCC AATATGAATA TCACCTCAGA
28701  TGAGAGTCTG GCCACTTCTA AAGCCACCAC GGAGACAGAG GCAATTCACG

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Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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28751	TTTTTGAAAA	TACAGCAGCG	TCCCATGTGG	AAACCACCAG	TGCTACAGAG
28801	GAACTCTATT	CCTCTTCCCC	AGGCTTCTCA	GAGCCAACAA	AAGTGATATC
28851	TCCAGTGGTC	ACCTCTTCCT	CTATAAGAGA	CAACATGGTT	TCCACAACAA
28901	TGCCTGGCTC	CTCTGGCATT	ACAAGGATTG	AGATAGAGTC	AATGTCATCT
28951	CTGACCCCTG	GACTGAGGGA	GACCAGAACC	TCCCAGGACA	TCACCTCATC
29001	CACAGAGACA	AGCACTGTCC	TTTACAAGAT	GTCCTCTGGT	GCCACTCCTG
29051	AGGTCTCCAG	GACAGAAGTT	ATGCCCTCTA	GCAGAACATC	CATTCTGGC
29101	CCTGCTCAGT	CCACAATGTC	ACTAGACATC	TCCGATGAAG	TTGTCACCAG
29151	GCTGTCTACC	TCTCCCATCA	TGACAGAATC	TGCAGAAATA	ACCATCACCA
29201	CCCAAACAGG	TTATTCTCTG	GCTACATCCC	AGGTTACCCT	TCCCTTGGGC
29251	ACCTCAATGA	CCTTTTTGTC	AGGGACCCAC	TCAACTATGT	CTCAAGGACT
29301	TTCACTCA	GAGATGACCA	ATCTTATGAG	CAGGGGTCCT	GAAAGTCTGT
29351	CATGGACGAG	CCCTCGCTTT	GTGGAAACAA	CTAGATCTTC	CTCTTCTCTG
29401	ACATCATTAC	CTCTCACGAC	CTCACTTTCT	CCTGTGTCCT	CCACATTACT
29451	AGACAGTAGC	CCCTCCTCTC	CTCTTCCTGT	GACTTCACTT	ATCCTCCCAG
29501	GCCTGGTGAA	GACTACAGAA	GTGTTGGATA	CAAGCTCAGA	GCCTAAAACC
29551	AGTTCATCTC	CAAATTTGAG	CAGCACCTCA	GTTGAAATAC	CGGCCACCTC
29601	TGAAATCATG	ACAGATACAG	AGAAAATTCA	TCCTTCTCTCA	AACACAGCGG
29651	TGGCCAAAGT	GAGGACCTCC	AGTTCTGTTC	ATGAATCTCA	TTCTCTGTC
29701	CTAGCTGACT	CAGAAACAAC	CATAACCATA	CCTTCAATGG	GTATCACCTC
29751	CGCTGTGGAC	GATACCACTG	TTTTCACATC	AAATCCTGCC	TTCTCTGAGA
29801	CTAGGAGGAT	TCCGACAGAG	CCAACATTCT	CATTGACTCC	TGGATTGAGG
29851	GAGACTAGCA	CCTCTGAAGA	GACCACCTCA	ATCACAGAAA	CAAGTGCAGT
29901	CCTTTATGGA	GTGCCCCTA	GTGCTACTAC	TGAAGTCTCC	ATGACAGAAA
29951	TCATGTCCTC	TAATAGAACA	CACATCCCTG	ACTCTGATCA	GTCCACGATG

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Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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30001	TCTCCAGACA	TCATCACTGA	AGTGATCACC	AGGCTCTCTT	CCTCATCCAT
30051	GATGTCAGAA	TCAACACAAA	TGACCATCAC	CACCCAAAAA	AGTTCTCCTG
30101	GGGCTACAGC	ACAGAGTACT	CTTACCTTGG	CCACAACAAC	AGCCCCCTTG
30151	GCAAGGACCC	ACTCAACTGT	TCCTCCTAGA	TTTTTACACT	CAGAGATGAC
30201	AACTCTTATG	AGTAGGAGTC	CTGAAAATCC	ATCATGGAAG	AGCTCTCCCT
30251	TTGTGGAAAA	AACTAGCTCT	TCATCTTCTC	TGTTGTCCTT	ACCTGTCACG
30301	ACCTCACCTT	CTGTTTCTTC	CACATTACCG	CAGAGTATCC	CTTCCTCCTC
30351	TTTTTCTGTG	ACTTCACTCC	TCACCCAGG	CATGGTGAAG	ACTACAGACA
30401	CAAGCACAGA	ACCTGGAACC	AGTTTATCTC	CAAATCTGAG	TGGCACCTCA
30451	GTTGAAATAC	TGGCTGCCTC	TGAAGTCACC	ACAGATACAG	AGAAAATTCA
30501	TCCTTCTTCA	AGCATGGCAG	TGACCAATGT	GGGAACCACC	AGTTCTGGAC
30551	ATGAACTATA	TTCCTCTGTT	TCAATCCACT	CGGAGCCATC	CAAGGCTACA
30601	TACCCAGTGG	GTACTCCCTC	TTCCATGGCT	GAAACCTCTA	TTTCCACATC
30651	AATGCCTGCT	AATTTTGAGA	CCACAGGATT	TGAGGCTGAG	CCATTTTCTC
30701	ATTTGACTTC	TGGATTTAGG	AAGACAAACA	TGTCCCTGGA	CACCAGCTCA
30751	GTCACACCAA	CAAATACACC	TTCTTCTCCT	GGGTCCACTC	ACCTTTTACA
30801	GAGTTCCAAG	ACTGATTTCA	CCTCTTCTGC	AAAAACATCA	TCCCCAGACT
30851	GGCCTCCAGC	CTCACAGTAT	ACTGAAATTC	CAGTGGACAT	AATCACCCCC
30901	TTTAATGCTT	CTCCATCTAT	TACGGAGTCC	ACTGGGATAA	CCTCCTTCCC
30951	AGAATCCAGG	TTTACTATGT	CTGTAACAGA	AAGTACTCAT	CATCTGAGTA
31001	CAGATTTGCT	GCCTTCAGCT	GAGACTATTT	CCACTGGCAC	AGTGATGCCT
31051	TCTCTATCAG	AGGCCATGAC	TTCATTTGCC	ACCACTGGAG	TTCCACGAGC
31101	CATCTCAGGT	TCAGGTAGTC	CATTCTCTAG	GACAGAGTCA	GGCCCTGGGG
31151	ATGCTACTCT	GTCCACCATT	GCAGAGAGCC	TGCCTTCATC	CACTCCTGTG
31201	CCATTCTCCT	CTTCAACCTT	CACTACCACT	GATTCTTCAA	CCATCCCAGC

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Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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31251	CCTCCATGAG	ATAACTTCCT	CTTCAGCTAC	CCCATATAGA	GTGGACACCA
31301	GTCTTGGGAC	AGAGAGCAGC	ACTACTGAAG	GACGCTTGGT	TATGGTCAGT
31351	ACTTTGGACA	CTTCAAGCCA	ACCAGGCAGG	ACATCTTCAA	CACCCATTTT
31401	GGATACCAGA	ATGACAGAGA	GCGTTGAGCT	GGGAACAGTG	ACAAGTGCTT
31451	ATCAAGTTCC	TTCACCTCTCA	ACACGGTTGA	CAAGAACTGA	TGGCATTATG
31501	GAACACATCA	CAAAAATACC	CAATGAAGCA	GCACACAGAG	GTACCATAAG
31551	ACCAGTCAAA	GGCCCTCAGA	CATCCACTTC	GCCTGCCAGT	CCTAAAGGAC
31601	TACACACAGG	AGGGACAAAA	AGAATGGAGA	CCACCACCAC	AGCTTTGAAG
31651	ACCACCACCA	CAGCTTTGAA	GACCACTTCC	AGAGCCACCT	TGACCACCAG
31701	TGTCTATACT	CCCACTTTGG	GAACACTGAC	TCCCCTCAAT	GCATCAAGGC
31751	AAATGGCCAG	CACAATCCTC	ACAGAAATGA	TGATCACAAC	CCCATATGTT
31801	TTCCCTGATG	TTCCAGAAAC	GACATCCTCA	TTGGCTACCA	GCCTGGGAGC
31851	AGAAACCAGC	ACAGCTCTTC	CCAGGACAAC	CCCATCTGTT	CTCAATAGAG
31901	AATCAGAGAC	CACAGCCTCA	CTGGTCTCTC	GTTCTGGGGC	AGAGAGAAGT
31951	CCGGTTATTTC	AAACTCTAGA	TGTTTCTTCT	AGTGAGCCAG	ATACAACAGC
32001	TTCATGGGTT	ATCCATCCTG	CAGAGACCAT	CCCAACTGTT	TCCAAGACAA
32051	CCCCCAATTT	TTTCCACAGT	GAATTAGACA	CTGTATCTTC	CACAGCCACC
32101	AGTCATGGGG	CAGACGTCAG	CTCAGCCATT	CCAACAAATA	TCTCACCTAG
32151	TGAACTAGAT	GCACTGACCC	CACTGGTCAC	TATTTTCGGGG	ACAGATACTA
32201	GTACAACATT	CCCAACACTG	ACTAAGTCCC	CACATGAAAC	AGAGACAAGA
32251	ACCACATGGC	TCACTCATCC	TGCAGAGACC	AGCTCAACTA	TTCCCAGAAC
32301	AATCCCCAAT	TTTTCTCATC	ATGAATCAGA	TGCCACACCT	TCAATAGCCA
32351	CCAGTCCTGG	GGCAGAAACC	AGTTCAGCTA	TTCCAATTAT	GACTGTCTCA
32401	CCTGGTGCAG	AAGATCTGGT	GACCTCACAG	GTCACTAGTT	CTGGGACAGA
32451	CAGAAATATG	ACTATTCCAA	CTTTGACTCT	TTCTCCTGGT	GAACCAAAGA

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Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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32501	CGATAGCCTC	ATTAGTCACC	CATCCTGAAG	CACAGACAAG	TTCGGCCATT
32551	CCAACTTCAA	CTATCTCGCC	TGCTGTATCA	CGGTTGGTGA	CCTCAATGGT
32601	CACCAGTTTG	GCGGCAAAGA	CAAGTACAAC	TAATCGAGCT	CTGACAAACT
32651	CCCCTGGTGA	ACCAGCTACA	ACAGTTTCAT	TGGTCACGCA	TCCTGCACAG
32701	ACCAGCCCAA	CAGTTCCTTG	GACAACTTCC	ATTTTTTTCC	ATAGTAAATC
32751	AGACACCACA	CCTTCAATGA	CCACCAGTCA	TGGGGCAGAA	TCCAGTTCAG
32801	CTGTTCCAAC	TCCAACGTGT	TCAACTGAGG	TACCAGGAGT	AGTGACCCCT
32851	TTGGTCACCA	GTTCTAGGGC	AGTGATCAGT	ACAACTATTTC	CAATTCTGAC
32901	TCTTTCTCCT	GGTGAACCAG	AGACCACACC	TTCAATGGCC	ACCAGTCATG
32951	GGGAAGAAGC	CAGTTCCTGCT	ATTCCAACCTC	CAACTGTTTC	ACCTGGGGTA
33001	CCAGGAGTGG	TGACCTCTCT	GGTCACTAGT	TCTAGGGCAG	TGACTAGTAC
33051	AACTATTCCA	ATTCTGACTT	TTTCTCTTGG	TGAACCAGAG	ACCACACCTT
33101	CAATGGCCAC	CAGTCATGGG	ACAGAAGCTG	GCTCAGCTGT	TCCAACGTGT
33151	TTACCTGAGG	TACCAGGAAT	GGTGACCTCT	CTGGTTGCTA	GTTCTAGGGC
33201	AGTAACCAGT	ACAACTCTTC	CAACTCTGAC	TCTTTCTCCT	GGTGAACCAG
33251	AGACCACACC	TTCAATGGCC	ACCAGTCATG	GGGCAGAAGC	CAGCTCAACT
33301	GTTCCAACCTG	TTTCACCTGA	GGTACCAGGA	GTGGTGACCT	CTCTGGTCAC
33351	TAGTTCTAGT	GGAGTAAACA	GTACAAGTAT	TCCAACCTCTG	ATTCTTTCTC
33401	CTGGTGAACT	AGAAACCACA	CCTTCAATGG	CCACCAGTCA	TGGGGCAGAA
33451	GCCAGCTCAG	CTGTTCCAAC	TCCAACGTGT	TCACCTGGGG	TATCAGGAGT
33501	GGTGACCCCT	CTGGTCACTA	GTTCCAGGGC	AGTGACCAGT	ACAACTATTTC
33551	CAATTCTAAC	TCTTTCTTCT	AGTGAGCCAG	AGACCACACC	TTCAATGGCC
33601	ACCAGTCATG	GGGTAGAAGC	CAGCTCAGCT	GTTCTAACTG	TTTCACCTGA
33651	GGTACCAGGA	ATGGTGACCT	CTCTGGTCAC	TAGTTCTAGA	GCAGTAACCA
33701	GTACAACTAT	TCCAACCTCTG	ACTATTTCTT	CTGATGAACC	AGAGACCACA

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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33751	ACTTCATTGG	TCACCCATTC	TGAGGCAAAG	ATGATTTCAG	CCATTCCAAC
33801	TTTAGCTGTC	TCCCCTACTG	TACAAGGGCT	GGTGACTTCA	CTGGTCACTA
33851	GTTCTGGGTC	AGAGACCAGT	GCGTTTTTCAA	ATCTAACTGT	TGCCTCAAGT
33901	CAACCAGAGA	CCATAGACTC	ATGGGTCGCT	CATCCTGGGA	CAGAAGCAAG
33951	TTCTGTTGTT	CCAAC TTGA	CTGTCTCCAC	TGGTGAGCCG	TTTACAAATA
34001	TCTCATTGGT	CACCCATCCT	GCAGAGAGTA	GCTCAACTCT	TCCCAGGACA
34051	ACCTCAAGGT	TTTCCCACAG	TGAATTAGAC	ACTATGCCTT	CTACAGTCAC
34101	CAGTCCTGAG	GCAGAATCCA	GCTCAGCCAT	TTCAACTACT	ATTTACCTG
34151	GTATACCAGG	TGTGCTGACA	TCACTGGTCA	CTAGCTCTGG	GAGAGACATC
34201	AGTGCAACTT	TTCCAACAGT	GCCTGAGTCC	CCACATGAAT	CAGAGGCAAC
34251	AGCCTCATGG	GTTACTCATC	CTGCAGTCAC	CAGCACAACA	GTTCCCAGGA
34301	CAACCCCTAA	TTATTCTCAT	AGTGAACCAG	ACACCACACC	ATCAATAGCC
34351	ACCAGTCCTG	GGGCAGAAGC	CACTTCAGAT	TTTCCAACAA	TAACTGTCTC
34401	ACCTGATGTA	CCAGATATGG	TAACCTCACA	GGTCACTAGT	TCTGGGACAG
34451	ACACCAGTAT	AACTATTCCA	ACTCTGACTC	TTTCTTCTGG	TGAGCCAGAG
34501	ACCACAACCT	CATTTATCAC	CTATTCTGAG	ACACACACAA	GTTCAGCCAT
34551	TCCAAC TCTC	CCTGTCTCCC	CTGGTGCATC	AAAGATGCTG	ACCTCACTGG
34601	TCATCAGTTC	TGGGACAGAC	AGCACTACAA	CTTTCCCAAC	ACTGACGGAG
34651	ACCCCATATG	AACCAGAGAC	AACAGCCATA	CAGCTCATTC	ATCCTGCAGA
34701	GACCAACACA	ATGGTTCCCA	AGACAACTCC	CAAGTTTTTCC	CATAGTAAGT
34751	CAGACACCAC	ACTCCCAGTA	GCCATCACCA	GTCCTGGGCC	AGAAGCCAGT
34801	TCAGCTGTTT	CAACGACAAC	TATCTCACCT	GATATGTCAG	ATCTGGTGAC
34851	CTCACTGGTC	CCTAGTTCTG	GGACAGACAC	CAGTACAACC	TTCCCAACAT
34901	TGAGTGAGAC	CCCATATGAA	CCAGAGACTA	CAGTCACGTG	GCTCACTCAT
34951	CCTGCAGAAA	CCAGCACAAC	GGTTTCTGGG	ACAATTCCCA	ACTTTTCCCA

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Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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35001	TAGGGGATCA	GACACTGCAC	CCTCAATGGT	CACCAGTCCT	GGAGTAGACA
35051	CGAGGTCAGG	TGTTCCAAC	ACAACCATCC	CACCCAGTAT	ACCAGGGGTA
35101	GTGACCTCAC	AGGTCAC	TTCTGCAACA	GACACTAGTA	CAGCTATTCC
35151	AACTTTGACT	CCTTCTCCTG	GTGAACCAGA	GACCACAGCC	TCATCAGCTA
35201	CCCATCCTGG	GACACAGACT	GGCTTCACTG	TTCCAATTCG	GACTGTTCCC
35251	TCTAGTGAGC	CAGATACAAT	GGCTTCCTGG	GTCAC	CTCCACAGAC
35301	CAGCACACCT	GTTTCCAGAA	CAACCTCCAG	TTTTTCCCAT	AGTAGTCCAG
35351	ATGCCACACC	TGTAATGGCC	ACCAGTCCTA	GGACAGAAGC	CAGTTCAGCT
35401	GTACTGACAA	CAATCTCACC	TGGTGCACCA	GAGATGGTGA	CTTCACAGAT
35451	CACTAGTTCT	GGGGCAGCAA	CCAGTACAAC	TGTTCCAAC	TTGACTCATT
35501	CTCCTGGTAT	GCCAGAGACC	ACAGCCTTAT	TGAGCACCCA	TCCCAGAACA
35551	GGGACAAGTA	AAACATTTCC	TGCTTCAACT	GTGTTTCCTC	AAGTATCAGA
35601	GACCACAGCC	TCACTCACCA	TTAGACCTGG	TGCAGAGACT	AGCACAGCTC
35651	TCCCAACTCA	GACAACATCC	TCTCTCTTCA	CCCTACTTGT	AACTGGAACC
35701	AGCAGAGTTG	ATCTAAGTCC	AACTGCTTCA	CCTGGTGTTT	CTGCAAAAAC
35751	AGCCCCACTT	TCCACCCATC	CAGGGACAGA	GACCAGCACA	ATGATTCCAA
35801	CTTCAACTCT	TTCCCTTGGT	TTACTAGAGA	CTACAGGCTT	ACTGGCCACC
35851	AGCTCTTCAG	CAGAGACCAG	CACGAGTACT	CTA	CTGTTTCCCC
35901	TGCTGTCTCT	GGGCTTTCCA	GTGCCTCTAT	AACA	AAGCCCCAAA
35951	CTGTGACCTC	CTGGAACACA	GAAACCTCAC	CATCTGTAAC	TTCAGTTGGA
36001	CCCCCAGAAT	TTTCCAGGAC	TGTCACAGGC	ACCACTATGA	CCTTGATACC
36051	ATCAGAGATG	CCAACACCAC	CTAAAACCAG	TCATGGAGAA	GGAGTGAGTC
36101	CAACCACTAT	CTTGAGAACT	ACAATGGTTG	AAGCCACTAA	TTTAGCTACC
36151	ACAGGTTC	GTCCCACTGT	GGCCAAGACA	ACAACCACCT	TCAATACACT
36201	GGCTGGAAGC	CTCTTTACTC	CTCTGACCAC	ACCTGGGATG	TCCACCTTGG

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Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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36251	CCTCTGAGAG	TGTGACCTCA	AGAACAAGTT	ATAACCATCG	GTCTTGATC
36301	TCCACCACCA	GCAGTTATAA	CCGTCGGTAC	TGGACCCCTG	CCACCAGCAC
36351	TCCAGTGACT	TCTACATTCT	CCCCAGGGAT	TTCCACATCC	TCCATCCCCA
36401	GCTCCACAGC	AGCCACAGTC	CCATTCATGG	TGCCATTAC	CCTCAACTTC
36451	ACCATCACCA	ACCTGCAGTA	CGAGGAGGAC	ATGCGGCACC	CTGGTTCCAG
36501	GAAGTTCAAC	GCCACAGAGA	GAGAACTGCA	GGGTCTGCTC	AAACCCTTGT
36551	TCAGGAATAG	CAGTCTGGAA	TACCTCTATT	CAGGCTGCAG	ACTAGCCTCA
36601	CTCAGGCCAG	AGAAGGATAG	CTCAGCCATG	GCAGTGGATG	CCATCTGCAC
36651	ACATCGCCCT	GACCCTGAAG	ACCTCGGACT	GGACAGAGAG	CGACTGTACT
36701	GGGAGCTGAG	CAATCTGACA	AATGGCATCC	AGGAGCTGGG	CCCCTACACC
36751	CTGGACCGGA	ACAGTCTCTA	TGTCAATGGT	TTCACCCATC	GAAGCTCTAT
36801	GCCCACCACC	AGCACTCCTG	GGACCTCCAC	AGTGGATGTG	GGAACCTCAG
36851	GGACTCCATC	CTCCAGCCCC	AGCCCCACGG	CTGCTGGCCC	TCTCCTGATG
36901	CCGTTACCCC	TCAACTTCAC	CATCACCAAC	CTGCAGTACG	AGGAGGACAT
36951	GCGTCGCACT	GGCTCCAGGA	AGTTCAACAC	CATGGAGAGT	GTCTGTCAGG
37001	GTCTGCTCAA	GCCCTTGTTT	AAGAACACCA	GTGTTGGCCC	TCTGTACTCT
37051	GGCTGCAGAT	TGACCTTGCT	CAGGCCCCGAG	AAAGATGGGG	CAGCCACTGG
37101	AGTGGATGCC	ATCTGCACCC	ACCGCCTTGA	CCCCAAAAGC	CCTGGACTCA
37151	ACAGGGAGCA	GCTGTACTGG	GAGCTAAGCA	AACTGACCAA	TGACATTGAA
37201	GAGCTGGGCC	CCTACACCCT	GGACAGGAAC	AGTCTCTATG	TCAATGGTTT
37251	CACCCATCAG	AGCTCTGTGT	CCACCACCAG	CACTCCTGGG	ACCTCCACAG
37301	TGGATCTCAG	AACCTCAGGG	ACTCCATCCT	CCCTCTCCAG	CCCCACAATT
37351	ATGGCTGCTG	GCCCTCTCCT	GGTACCATTC	ACCCTCAACT	TCACCATCAC
37401	CAACCTGCAG	TATGGGGAGG	ACATGGGTCA	CCCTGGCTCC	AGGAAGTTCA
37451	ACACCACAGA	GAGGGTCCTG	CAGGGTCTGC	TTGGTCCCAT	ATTCAAGAAC

Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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37501	ACCAGTGTG	GCCCTCTGTA	CTCTGGCTGC	AGACTGACCT	CTCTCAGGTC
37551	TGAGAAGGAT	GGAGCAGCCA	CTGGAGTGGA	TGCCATCTGC	ATCCATCATC
37601	TTGACCCCAA	AAGCCCTGGA	CTCAACAGAG	AGCGGCTGTA	CTGGGAGCTG
37651	AGCCAACTGA	CCAATGGCAT	CAAAGAGCTG	GGCCCCTACA	CCCTGGACAG
37701	GAACAGTCTC	TATGTCAATG	GTTTCACCCA	TCGGACCTCT	GTGCCCACCA
37751	CCAGCACTCC	TGGGACCTCC	ACAGTGGACC	TTGGAACCTC	AGGGACTCCA
37801	TTCTCCCTCC	CAAGCCCCGC	AACTGCTGGC	CCTCTCCTGG	TGCTGTTTAC
37851	CCTCAACTTC	ACCATCACCA	ACCTGAAGTA	TGAGGAGGAC	ATGCATCGCC
37901	CTGGCTCCAG	GAAGTTCAAC	ACCACTGAGA	GGGTCCTGCA	GACTCTGCTT
37951	GGTCCTATGT	TCAAGAACAC	CAGTGTGGC	CTTCTGTACT	CTGGCTGCAG
38001	ACTGACCTTG	CTCAGGTCCG	AGAAGGATGG	AGCAGCCACT	GGAGTGGATG
38051	CCATCTGCAC	CCACCGTCTT	GACCCCAAAA	GCCCTGGACT	GGACAGAGAG
38101	CAGCTATACT	GGGAGCTGAG	CCAGCTGACC	AATGGCATCA	AAGAGCTGGG
38151	CCCCTACACC	CTGGACAGGA	ACAGTCTCTA	TGTCAATGGT	TTCACCCATT
38201	GGATCCCTGT	GCCCACCAGC	AGCACTCCTG	GGACCTCCAC	AGTGGACCTT
38251	GGGTCAGGGA	CTCCATCCTC	CCTCCCCAGC	CCCACAGCTG	CTGGCCCTCT
38301	CCTGGTGCCA	TTCACCCTCA	ACTTCACCAT	CACCAACCTG	CAGTACGAGG
38351	AGGACATGCA	TCACCCAGGC	TCCAGGAAGT	TCAACACCAC	GGAGCGGGTC
38401	CTGCAGGGTC	TGCTTGGTCC	CATGTTCAAG	AACACCAGTG	TCGGCCTTCT
38451	GTA CTCTGGC	TGCAGACTGA	CCTTGCTCAG	GTCCGAGAAG	GATGGAGCAG
38501	CCACTGGAGT	GGATGCCATC	TGCACCCACC	GTCTTGACCC	CAAAAGCCCT
38551	GGAGTGGACA	GGGAGCAGCT	ATACTGGGAG	CTGAGCCAGC	TGACCAATGG
38601	CATCAAAGAG	CTGGGTCCCT	ACACCCTGGA	CAGAAACAGT	CTCTATGTCA
38651	ATGGTTTCAC	CCATCAGACC	TCTGCGCCCA	ACACCAGCAC	TCCTGGGACC
38701	TCCACAGTGG	ACCTGGGGAC	CTCAGGGACT	CCATCCTCCC	TCCCCAGCCC

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Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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38751	TACATCNGCT	GGCCCTCTCC	TGGTNCCNTT	CACCCTCAAC	TTCACCATCA
38801	CCAACCTGCA	GTACGAGGAG	GACATGCGGC	ACCCNGGNTC	CAGGAAGTTC
38851	AACACCACNG	AGAGGGTNCT	GCAGGGTCTG	CTNAAGCCCC	TNTTCAAGAG
38901	CACCAGTGTT	GGCCCTCTGT	ACTCTGGCTG	CAGACTGACC	TTGCTCAGGT
38951	CCGAGAAGGA	TGGAGCAGCC	ACTGGAGTGG	ATGCCATCTG	CACCCACCGT
39001	CTTGACCCCA	AAAGCCCTGG	AGTGGACAGG	GAGCAGCTAT	ACTGGGAGCT
39051	GAGCCAGCTG	ACCAATGGCA	TCAAAGAGCT	GGGTCCCTAC	ACCCTGGACA
39101	GAAACAGTCT	CTATGTCAAT	GGTTTCACCC	ATCAGACCTC	TGCGCCCAAC
39151	ACCAGCACTC	CTGGGACCTC	CACAGTGGAC	CTTGGGACCT	CAGGGACTCC
39201	ATCCTCCCTC	CCCAGCCCTA	CATCTGCTGG	CCCTCTCCTG	GTGCCATTCA
39251	CCCTCAACTT	CACCATCACC	AACCTGCAGT	ACGAGGAGGA	CATGCATCAC
39301	CCAGGCTCCA	GGAAGTTCAA	CACCACGGAG	CGGGTCCTGC	AGGGTCTGCT
39351	TGGTCCCATG	TTCAAGAACA	CCAGTGTCCG	CCTTCTGTAC	TCTGGCTGCA
39401	GA CTGACCTT	GCTCAGGCCT	GAGAAGAATG	GGGCAGCCAC	TGGAATGGAT
39451	GCCATCTGCA	GCCACCGTCT	TGACCCCAA	AGCCCTGGAC	TCAACAGAGA
39501	GCAGCTGTAC	TGGGAGCTGA	GCCAGCTGAC	CCATGGCATC	AAAGAGCTGG
39551	GCCCCTACAC	CCTGGACAGG	AACAGTCTCT	ATGTCAATGG	TTTCACCCAT
39601	CGGAGCTCTG	TGGCCCCCAC	CAGCACTCCT	GGGACCTCCA	CAGTGGACCT
39651	TGGGACCTCA	GGGACTCCAT	CCTCCCTCCC	CAGCCCCACA	ACAGCTGTTC
39701	CTCTCCTGGT	GCCGTTACAC	CTCAACTTTA	CCATCACCAA	TCTGCAGTAT
39751	GGGGAGGACA	TGCGTCACCC	TGGCTCCAGG	AAGTTCAACA	CCACAGAGAG
39801	GGTCCTGCAG	GGTCTGCTTG	GTCCCTTGTT	CAAGAACTCC	AGTGTGCGCC
39851	CTCTGTACTC	TGGCTGCAGA	CTGATCTCTC	TCAGGTCTGA	GAAGGATGGG
39901	GCAGCCACTG	GAGTGGATGC	CATCTGCACC	CACCACCTTA	ACCCTCAAAG
39951	CCCTGGACTG	GACAGGGAGC	AGCTGTACTG	GCAGCTGAGC	CAGATGACCA

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Table 4 (continued)

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**Human cDNA of CA125**  
(SEQ ID NO: 4)

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40001	ATGGCATCAA	AGAGCTGGGC	CCCTACACCC	TGGACCGGAA	CAGTCTCTAC
40051	GTCAATGGTT	TCACCCATCG	GAGCTCTGGG	CTCACCACCA	GCACTCCTTG
40101	GACTTCCACA	GTTGACCTTG	GAACCTCAGG	GACTCCATCC	CCCGTCCCCA
40151	GCCCCACAAC	TGCTGGCCCT	CTCCTGGTGC	CATTCACCCT	CAACTTCACC
40201	ATCACCAACC	TGCAGTATGA	GGAGGACATG	CATCGCCCTG	GATCTAGGAA
40251	GTTCAACACC	ACAGAGAGGG	TCCTGCAGGG	TCTGCTTAGT	CCCATTTTCA
40301	AGAACTCCAG	TGTTGGCCCT	CTGTACTCTG	GCTGCAGACT	GACCTCTCTC
40351	AGGCCCCGAGA	AGGATGGGGC	AGCAACTGGA	ATGGATGCTG	TCTGCCTCTA
40401	CCACCCTAAT	CCCAAAAGAC	CTGGACTGGA	CAGAGAGCAG	CTGTACTGGG
40451	AGCTAAGCCA	GCTGACCCAC	AACATCACTG	AGCTGGGCCC	CTACAGCCTG
40501	GACAGGGACA	GTCTCTATGT	CAATGGTTTC	ACCCATCAGA	ACTCTGTGCC
40551	CACCACCAGT	ACTCCTGGGA	CCTCCACAGT	GTACTGGGCA	ACCACTGGGA
40601	CTCCATCCTC	CTTCCCCGGC	CACACAGAGC	CTGGCCCTCT	CCTGATACCA
40651	TTCACTTTCA	ACTTTACCAT	CACCAACCTG	ATTATGAGG	AAAACATGCA
40701	ACACCCTGGT	TCCAGGAAGT	TCAACACCAC	GGAGAGGGTT	CTGCAGGGTC
40751	TGCTCAAGCC	CTTGTTCAAG	AACACCAGTG	TTGGCCCTCT	GTACTCTGGC
40801	TGCAGACTGA	CCTCTCTCAG	GCCCGAGAAG	GATGGGGCAG	CAACTGGAAT
40851	GGATGCTGTC	TGCCTCTACC	ACCCTAATCC	CAAAAGACCT	GGGCTGGACA
40901	GAGAGCAGCT	GTACTGGGAG	CTAAGCCAGC	TGACCCACAA	CATCACTGAG
40951	CTGGGCCCCCT	ACAGCCTGGA	CAGGGACAGT	CTCTATGTCA	ATGGTTTCAC
41001	CCATCAGAAC	TCTGTGCCCA	CCACCAGTAC	TCCTGGGACC	TCCACAGTGT
41051	ACTGGGCAAC	CACTGGGACT	CCATCCTCCT	TCCCCGGCCA	CACAGAGCCT
41101	GGCCCTCTCC	TGATACCATT	CACTTTCAAC	TTTACCATCA	CCAACCTGCA
41151	TTATGAGGAA	AACATGCAAC	ACCCTGGTTC	CAGGAAGTTC	AACACCACGG
41201	AGAGGGTTCT	GCAGGGTCTG	CTCAAGCCCT	TGTTCAAGAA	CACCAGTGTT

Table 4 (continued)

## Human cDNA of CA125

(SEQ ID NO: 4)

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41251  GGCCCTCTGT ACTCTGGCTG CAGACTGACC TTGCTCAGAC CTGAGAAGCA
41301  TGAGGCAGCC ACTGGAGTGG ACACCATCTG TACCCACCGC GTTGATCCCA
41351  TCGGACCTGG ACTGGACAGG GAGCGGCTAT ACTGGGAGCT GAGCCAGCTG
41401  ACCAACAGCA TTACCGAACT GGGACCCTAC ACCCTGGACA GGGACAGTCT
41451  CTATGTCAAT GGCTTCAACC CTCGGAGCTC TGTGCCAACC ACCAGCACTC
41501  CTGGGACCTC CACAGTGCAC CTGGCAACCT CTGGGACTCC ATCCTCCCTG
41551  CCTGGCCACA CAGCCCCTGT CCCTCTCTTG ATACCATTCA CCCTCAACTT
41601  TACCATCACC AACCTGCATT ATGAGGAAAA CATGCAACAC CCTGGTTCCA
41651  GGAAGTTCAA CACCACGGAG AGGGTTCTGC AGGGTCTGCT CAAGCCCTTG
41701  TTCAAGAACA CCAGTGTGG CCCTCTGTAC TCTGGCTGCA GACTGACCTT
41751  GCTCAGACCT GAGAAGCATG AGGCAGCCAC TGGAGTGGAC ACCATCTGTA
41801  CCCACCGCGT TGATCCCATC GGACCTGGAC TGNACAGNGA GCNGCTNTAC
41851  TGGGAGCTNA GCCANCTGAC CAANNNCATC NNGAGCTGG GNCCCTACAC
41901  CCTGGACAGG NACAGTCTCT ATGTCAATGG TTTCACCCAT CNGANCTCTG
41951  NGCCCACCAC CAGCACTCCT GGGACCTCCA CAGTGNACNT NGGNACCTCN
42001  GGGACTCCAT CCTCCNTCCC CNGCCNCACA TCTGCTGGCC CTCTCCTGGT
42051  GCCATTCACC CTCAACTTCA CCATCACCAA CCTGCAGTAC GAGGAGGACA
42101  TGCATCACCC AGGCTCCAGG AAGTTCAACA CCACGGAGCG GGTCTGTCAG
42151  GGTCTGCTTG GTCCCATGTT CAAGAACACC AGTGTCGGCC TTCTGTACTC
42201  TGGCTGCAGA CTGACCTTGC TCAGGCCTGA GAAGAATGGG GCAGCCACTG
42251  GAATGGATGC CATCTGCAGC CACCGTCTTG ACCCCAAAAG CCCTGGACTC
42301  GACAGAGAGC AGCTGTACTG GGAGCTGAGC CAGCTGACCC ATGGCATCAA
42351  AGAGCTGGGC CCCTACACCC TGGACAGGAA CAGTCTCTAT GTCAATGGTT
42401  TCACCCATCG GAGCTCTGTG GCCCCACCA GCACTCCTGG GACCTCCACA
42451  GTGGACCTTG GGACCTCAGG GACTCCATCC TCCCTCCCCA GCCCCACAAC

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Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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42501	AGCTGTTCCCT	CTCCTGGTGC	CGTTCACCCT	CAACTTTACC	ATCACCAATC
42551	TGCAGTATGG	GGAGGACATG	CGTCACCCTG	GCTCCAGGAA	GTTCAACACC
42601	ACAGAGAGGG	TCCTGCAGGG	TCTGCTTGGT	CCCTTGTTCA	AGAACTCCAG
42651	TGTCGGCCCT	CTGTACTCTG	GCTGCAGACT	GATCTCTCTC	AGGTCTGAGA
42701	AGGATGGGGC	AGCCACTGGA	GTGGATGCCA	TCTGCACCCA	CCACCTTAAC
42751	CCTCAAAGCC	CTGGACTGGA	CAGGGAGCAG	CTGTACTGGC	AGCTGAGCCA
42801	GATGACCAAT	GGCATCAAAG	AGCTGGGCCC	CTACACCCTG	GACCGGAACA
42851	GTCTCTACGT	CAATGGTTTC	ACCCATCGGA	GCTCTGGGCT	CACCACCAGC
42901	ACTCCTTGGA	CTTCCACAGT	TGACCTTGGA	ACCTCAGGGA	CTCCATCCCC
42951	CGTCCCCAGC	CCCACAAGT	CTGGCCCTCT	CCTGGTGCCA	TTCACCCTAA
43001	ACTTCACCAT	CACCAACCTG	CAGTATGAGG	AGGACATGCA	TCGCCCTGGA
43051	TCTAGGAAGT	TCAACGCCAC	AGAGAGGGTC	CTGCAGGGTC	TGCTTAGTCC
43101	CATATTCAAG	AACTCCAGTG	TTGGCCCTCT	GTACTCTGGC	TGCAGACTGA
43151	CCTCTCTCAG	GCCCGAGAAG	GATGGGGCAG	CAACTGGAAT	GGATGCTGTC
43201	TGCCTCTACC	ACCCTAATCC	CAAAAGACCT	GGACTGGACA	GAGAGCAGCT
43251	GTAAGGGAG	CTAAGCCAGC	TGACCCACAA	CATCACTGAG	CTGGGCCCCCT
43301	ACAGCCTGGA	CAGGGACAGT	CTCTATGTCA	ATGGTTTCAC	CCATCAGAGC
43351	TCTATGACGA	CCACCAGAAC	TCCTGATACC	TCCACAATGC	ACCTGGCAAC
43401	CTCGAGAACT	CCAGCCTCCC	TGTCTGGACC	TACGACCGCC	AGCCCTCTCC
43451	TGGTGCTATT	CACAATCAAC	TGCACCATCA	CCAACCTGCA	GTACGAGGAG
43501	GACATGCGTC	GCACTGGCTC	CAGGAAGTTC	AACACCATGG	AGAGTGTCTT
43551	GCAGGGTCTG	CTCAAGCCCT	TGTTCAAGAA	CACCAGTGTT	GGCCCTCTGT
43601	ACTCTGGCTG	CAGATTGACC	TTGCTCAGGC	CCAAGAAAGA	TGGGGCAGCC
43651	ACTGGAGTGG	ATGCCATCTG	CACCCACCGC	CTTGACCCCA	AAAGCCCTGG
43701	ACTCAACAGG	GAGCAGCTGT	ACTGGGAGCT	AAGCAAAGTG	ACCAATGACA

Table 4 (continued)

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**Human cDNA of CA125**  
(SEQ ID NO: 4)

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43751	TTGAAGAGCT	GGGCCCCTAC	ACCCTGGACA	GGAACAGTCT	CTATGTCAAT
43801	GGTTTCACCC	ATCAGAGCTC	TGTGTCCACC	ACCAGCACTC	CTGGGACCTC
43851	CACAGTGGAT	CTCAGAACCT	CAGGGACTCC	ATCCTCCCTC	TCCAGCCCCA
43901	CAATTATGNC	NNCTGNCCCT	CTCCTGNTNC	CNTTCACCNT	CAACTTNACC
43951	ATCACCAACC	TGCANTANGN	GGANNACATG	CNNCNCNCNG	GNTCCAGGAA
44001	GTTCAACACC	ACNGAGAGGG	TCCTACAGGG	TCTGCTCAGG	CCCTTGTTCA
44051	AGAACACCAG	TGTCAGCTCT	CTGTACTCTG	GTTGCAGACT	GACCTTGCTC
44101	AGGCCTGAGA	AGGATGGGGC	AGCCACCAGA	GTGGATGCTG	CCTGCACCTA
44151	CCGCCCTGAT	CCCAAAAGCC	CTGGACTGGA	CAGAGAGCAA	CTATACTGGG
44201	AGCTGAGCCA	GCTAACCAC	AGCATCACTG	AGCTGGGACC	CTACACCCTG
44251	GACAGGGTCA	GTCTCTATGT	CAATGGCTTC	AACCCTCGGA	GCTCTGTGCC
44301	AACCACCAGC	ACTCCTGGGA	CCTCCACAGT	GCACCTGGCA	ACCTCTGGGA
44351	CTCCATCCTC	CCTGCCTGGC	CACACANCNN	CTGNCCCTCT	CCTGNTNCCN
44401	TTCACCNTCA	ACTTNACCAT	CACCAACCTG	CANTANGNGG	ANNACATGCN
44451	NCNCCCNGGN	TCCAGGAAGT	TCAACACCAC	NGAGAGGGTT	CTGCAGGGTC
44501	TGCTCAAACC	CTTGTTTCAGG	AATAGCAGTC	TGGAATACCT	CTATTCAGGC
44551	TGCAGACTAG	CCTCACTCAG	GCCAGAGAAG	GATAGCTCAG	CCATGGCAGT
44601	GGATGCCATC	TGCACACATC	GCCCTGACCC	TGAAGACCTC	GGACTGGACA
44651	GAGAGCGACT	GTACTGGGAG	CTGAGCAATC	TGACAAATGG	CATCCAGGAG
44701	CTGGGCCCCCT	ACACCCTGGA	CCGGAACAGT	CTCTACGTCA	ATGGTTTCAC
44751	CCATCGGAGC	TCTGGGCTCA	CCACCAGCAC	TCCTTGGA	CTTCCAGTTG
44801	ACCTTGGAAC	CTCAGGGACT	CCATCCCCCG	TCCCCAGCCC	CACAACTGCT
44851	GGCCCTCTCC	TGGTGCCATT	CACCCTCAAC	TTCACCATCA	CCAACCTGCA
44901	GTATGAGGAG	GACATGCATC	GCCCTGGTTC	CAGGAGGTTC	AACACCACGG
44951	AGAGGGTTCT	GCAGGGTCTG	CTCACGCCCT	TGTTCAAGAA	CACCAGTGTT

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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45001	GGCCCTCTGT	ACTCTGGCTG	CAGACTGACC	TTGCTCAGAC	CTGAGAAGCA
45051	AGAGGCAGCC	ACTGGAGTGG	ACACCATCTG	TACCCACCGC	GTTGATCCCA
45101	TCGGACCTGG	ACTGGACAGA	GAGCGGCTAT	ACTGGGAGCT	GAGCCAGCTG
45151	ACCAACAGCA	TCACAGAGCT	GGGACCCTAC	ACCCTGGATA	GGGACAGTCT
45201	CTATGTCAAT	GGCTTCAACC	CTTGGAGCTC	TGTGCCAACC	ACCAGCACTC
45251	CTGGGACCTC	CACAGTGCAC	CTGGCAACCT	CTGGGACTCC	ATCCTCCCTG
45301	CCTGGCCACA	CAGCCCCTGT	CCCTCTCTTG	ATACCATTCA	CCCTCAACTT
45351	TACCATCACC	GACCTGCATT	ATGAAGAAAA	CATGCAACAC	CCTGGTTCCA
45401	GGAAGTTCAA	CACCACGGAG	AGGGTTCTGC	AGGGTCTGCT	CAAGCCCTTG
45451	TTCAAGAGCA	CCAGCGTTGG	CCCTCTGTAC	TCTGGCTGCA	GACTGACCTT
45501	GCTCAGACCT	GAGAAACATG	GGGCAGCCAC	TGGAGTGGAC	GCCATCTGCA
45551	CCCTCCGCCT	TGATCCCCT	GGTCCTGGAC	TGGACAGAGA	GCGGCTATAC
45601	TGGGAGCTGA	GCCAGCTGAC	CAACAGCGTT	ACAGAGCTGG	GCCCCTACAC
45651	CCTGGACAGG	GACAGTCTCT	ATGTCAATGG	CTTCACCCAT	CGGAGCTCTG
45701	TGCCAACCAC	CAGTATTCTT	GGGACCTCTG	CAGTGCACCT	GGAAACCTCT
45751	GGGACTCCAG	CCTCCCTCCC	TGGCCACACA	GCCCCTGGCC	CTCTCCTGGT
45801	GCCATTCAAC	CTCAACTTCA	CTATCACCAA	CCTGCAGTAT	GAGGAGGACA
45851	TGCGTCACCC	TGGTTCCAGG	AAGTTCAGCA	CCACGGAGAG	AGTCCTGCAG
45901	GGTCTGCTCA	AGCCCTTGTT	CAAGAACACC	AGTGTGAGCT	CTCTGTACTC
45951	TGGTTGCAGA	CTGACCTTGC	TCAGGCCTGA	GAAGGATGGG	GCAGCCACCA
46001	GAGTGGATGC	TGTCTGCACC	CATCGTCCTG	ACCCCAAAG	CCCTGGACTG
46051	GACAGAGAGC	GGCTGTACTG	GAAGCTGAGC	CAGCTGACCC	ACGGCATCAC
46101	TGAGCTGGGC	CCCTACACCC	TGGACAGGCA	CAGTCTCTAT	GTCAATGGTT
46151	TCACCCATCA	GAGCTCTATG	ACGACCACCA	GAACTCCTGA	TACCTCCACA
46201	ATGCACCTGG	CAACCTCGAG	AACTCCAGCC	TCCCTGTCTG	GACCTACGAC

Table 4 (continued)

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**Human cDNA of CA125**  
(SEQ ID NO: 4)

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46251	CGCCAGCCCT	CTCCTGGTGC	TATTCACAAT	TAAC TTCACC	ATCACTAACC
46301	TGCGGTATGA	GGAGAACATG	CATCACCCCTG	GCTCTAGAAA	GTTTAACACC
46351	ACGGAGAGAG	TCCTTCAGGG	TCTGCTCAGG	CCTGTGTTCA	AGAACACCAG
46401	TGTTGGCCCT	CTGTACTCTG	GCTGCAGACT	GACCACGCTC	AGGCCCAAGA
46451	AGGATGGGGC	AGCCACCAAA	GTGGATGCCA	TCTGCACCTA	CCGCCCTGAT
46501	CCCAAAGCC	CTGGACTGGA	CAGAGAGCAG	CTATACTGGG	AGCTGAGCCA
46551	GCTAACCAC	AGCATCACTG	AGCTGGGCCC	CTACACCCAG	GACAGGGACA
46601	GTCTCTATGT	CAATGGCTTC	ACCCATCGGA	GCTCTGTGCC	AACCACCAGT
46651	ATTCCTGGGA	CCTCTGCAGT	GCACCTGGAA	ACCTCTGGGA	CTCCAGCCTC
46701	CCTCCCTGGC	CACACAGCCC	CTGGCCCTCT	CCTGGTGCCA	TTCACCCTCA
46751	ACTTCACTAT	CACCAACCTG	CAGTATGAGG	AGGACATGCG	TCACCCTGGT
46801	TCCAGGAAGT	TCAACACCAC	GGAGAGAGTC	CTGCAGGGTC	TGCTCAAGCC
46851	CTTGTTCAAG	AGCACCAGTG	TTGGCCCTCT	GTA CTCTGGC	TGCAGACTGA
46901	CCTTGCTCAG	GCCTGAAAAA	CGTGGGGCAG	CCACCGGCGT	GGACACCATC
46951	TGCACTCACC	GCCTTGACCC	TCTAAACCCA	GGACTGGACA	GAGAGCAGCT
47001	ATACTGGGAG	CTGAGCAAAC	TGACCCGTGG	CATCATCGAG	CTGGGCCCCT
47051	ACCTCCTGGA	CAGAGGCAGT	CTCTATGTCA	ATGGTTTCAC	CCATCGGACC
47101	TCTGTGCCCA	CCACCAGCAC	TCCTGGGACC	TCCACAGTGG	ACCTTGGAAC
47151	CTCAGGGACT	CCATTCTCCC	TCCAAGCCC	CGCANCNNCT	GNCCCTCTCC
47201	TGNTNCCNTT	CACNTCAAC	TTNACCATCA	CCAACCTGCA	NTANGNGGAN
47251	NACATGCNNC	NCCNNGGNTC	CAGGAAGTTC	AACACCACNG	AGAGGGTCCT
47301	GCAGACTCTG	CTTGGTCCTA	TGTTCAAGAA	CACCAGTGTT	GGCCTTCTGT
47351	ACTCTGGCTG	CAGACTGACC	TTGCTCAGGT	CCGAGAAGGA	TGGAGCAGCC
47401	ACTGGAGTGG	ATGCCATCTG	CACCCACCGT	CTTGACCCCA	AAAGCCCTGG
47451	AGTGGACAGG	GAGCAACTAT	ACTGGGAGCT	GAGCCAGCTG	ACCAATGGCA

Table 4 (continued)

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**Human cDNA of CA125**  
(SEQ ID NO: 4)

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47501	TTAAAGAACT	GGGCCCCTAC	ACCCTGGACA	GGAACAGTCT	CTATGTCAAT
47551	GGGTTCACCC	ATTGGATCCC	TGTGCCCACC	AGCAGCACTC	CTGGGACCTC
47601	CACAGTGGAC	CTTGGGTCAG	GGACTCCATC	CTCCCTCCCC	AGCCCCACAA
47651	CTGCTGGCCC	TCTCCTGGTG	CCGTTACCCC	TCAACTTCAC	CATCACCAAC
47701	CTGAAGTACG	AGGAGGACAT	GCATTGCCCT	GGCTCCAGGA	AGTTCAACAC
47751	CACAGAGAGA	GTCCTGCAGA	GTCTGCTTGG	TCCCATGTTC	AAGAACACCA
47801	GTGTTGGCCC	TCTGTACTCT	GGCTGCAGAC	TGACCTTGCT	CAGGTCCGAG
47851	AAGGATGGAG	CAGCCACTGG	AGTGGATGCC	ATCTGCACCC	ACCGTCTTGA
47901	CCCCAAAAGC	CCTGGAGTGG	ACAGGGAGCA	GCTATACTGG	GAGCTGAGCC
47951	AGCTGACCAA	TGGCATCAAA	GAGCTGGGTC	CCTACACCCT	GGACAGAAAC
48001	AGTCTCTATG	TCAATGGTTT	CACCCATCAG	ACCTCTGCGC	CCAACACCAG
48051	CACTCCTGGG	ACCTCCACAG	TGGACCTTGG	GACCTCAGGG	ACTCCATCCT
48101	CCCTCCCCAG	CCCTACANCN	NCTGNCCCTC	TCCTGNTNCC	NTTCACCNTC
48151	AACTTNACCA	TCACCAACCT	GCANTANGNG	GANNACATGC	NNCNCNCNGG
48201	NTCCAGGAAG	TTCAACACCA	CNGAGNGNGT	NCTGCAGGGT	CTGCTNNNNC
48251	CCNTNTTCAA	GAACNCCAGT	GTNGGCCNTC	TGTA CTCTGG	CTGCAGACTG
48301	ACCTNNCTCA	GGNCNGAGAA	GNATGGNGCA	GCCACTGGAN	TGGATGCCAT
48351	CTGCANCCAG	CNNCNTNANC	CCAAAAGNCC	TGGACTGNAC	AGNGAGCNGC
48401	TN TACTGGGA	GCTNAGCCAN	CTGACCAANN	NCATCNNNGA	GCTGGGNCCC
48451	TACACCCTGG	ACAGGNACAG	TCTCTATGTC	AATGGTTTCA	CCCATTGGAT
48501	CCCTGTGCCC	ACCAGCAGCA	CTCCTGGGAC	CTCCACAGTG	GACCTTGGGT
48551	CAGGGACTCC	ATCCTCCCTC	CCCAGCCCCA	CAACTGCTGG	CCCTCTCCTG
48601	GTGCCGTTCA	CCCTCAACTT	CACCATCACC	AACCTGAAGT	ACGAGGAGGA
48651	CATGCATTGC	CCTGGCTCCA	GGAAGTTCAA	CACCACAGAG	AGAGTCCTGC
48701	AGAGTCTGCT	TGGTCCCATG	TTCAAGAACA	CCAGTGTTGG	CCCTCTGTAC

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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48751	TCTGGCTGCA	GACTGACCTC	GCTCAGGTCC	GAGAAGGATG	GAGCAGCCAC
48801	TGGAGTGGAT	GCCATCTGCA	CCCACCGTGT	TGACCCCAAA	AGCCCTGGAG
48851	TGGACAGGGA	GCAGCTATAC	TGGGAGCTGA	GCCAGCTGAC	CAATGGCATC
48901	AAAGAGCTGG	GTCCCTACAC	CCTGGACAGA	AACAGTCTCT	ATGTCAATGG
48951	TTTCACCCAT	CAGACCTCTG	CGCCCAACAC	CAGCACTCCT	GGGACCTCCA
49001	CAGTGNACNT	NGGNACCTCN	GGGACTCCAT	CCTCCNTCCC	CNGCCNCACA
49051	TCTGCTGGCC	CTCTCCTGGT	GCCATTCACC	CTCAACTTCA	CCATCACCAA
49101	CCTGCAGTAC	GAGGAGGACA	TGCATCACCC	AGGCTCCAGG	AAGTTCAACA
49151	CCACGGAGCG	GGTCCTGCAG	GGTCTGCTTG	GTCCCATGTT	CAAGAACACC
49201	AGTGTGGGCC	TTCTGTACTC	TGGCTGCAGA	CTGACCTTGC	TCAGGCCTGA
49251	GAAGAATGGG	GCAACCACTG	GAATGGATGC	CATCTGCACC	CACCGTCTTG
49301	ACCCCAAAAG	CCCTGGACTG	NACAGNGAGC	NGCTNTACTG	GGAGCTNAGC
49351	CANCTGACCA	ANNNCATCNN	NGAGCTGGGN	CCCTACACCC	TGGACAGGNA
49401	CAGTCTCTAT	GTCAATGGTT	TCACCCATCN	GANCTCTGNG	CCCACCACCA
49451	GCACTCCTGG	GACCTCCACA	GTGNACNTNG	GNACCTCNGG	GACTCCATCC
49501	TCCNTCCCCN	GCCNCACANC	NNCTGNCCCT	CTCCTGNTNC	CNTTCACCNT
49551	CAACTTNACC	ATCACCAACC	TGCANTANGN	GGANNACATG	CNNCNCNCNG
49601	GNTCCAGGAA	GTTCAACACC	ACNGAGAGGG	TTCTGCAGGG	TCTGCTCAAA
49651	CCCTTGTTCA	GGAATAGCAG	TCTGGAATAC	CTCTATTGAG	GCTGCAGACT
49701	AGCCTCACTC	AGGCCAGAGA	AGGATAGCTC	AGCCATGGCA	GTGGATGCCA
49751	TCTGCACACA	TCGCCCTGAC	CCTGAAGACC	TCGGACTGGA	CAGAGAGCGA
49801	CTGTACTGGG	AGCTGAGCAA	TCTGACAAAT	GGCATCCAGG	AGCTGGGCCC
49851	CTACACCCTG	GACCGGAACA	GTCTCTATGT	CAATGGTTTC	ACCCATCGAA
49901	GCTCTATGCC	CACCACCAGC	ACTCCTGGGA	CCTCCACAGT	GGATGTGGGA
49951	ACCTCAGGGA	CTCCATCCTC	CAGCCCCAGC	CCCACGACTG	CTGGCCCTCT



Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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50001	CCTGATACCA	TTCACCCTCA	ACTTCACCAT	CACCAACCTG	CAGTATGGGG
50051	AGGACATGGG	TCACCCTGGC	TCCAGGAAGT	TCAACACCAC	AGAGAGGGTC
50101	CTGCAGGGTC	TGCTTGGTCC	CATATTCAAG	AACACCAGTG	TTGGCCCTCT
50151	GTACTCTGGC	TGCAGACTGA	CCTCTCTCAG	GTCTGAGAAG	GATGGAGCAG
50201	CCACTGGAGT	GGATGCCATC	TGCATCCATC	ATCTTGACCC	CAAAAGCCCT
50251	GGACTCAACA	GAGAGCGGCT	GTACTGGGAG	CTGAGCCAAC	TGACCAATGG
50301	CATCAAAGAG	CTGGGCCCCCT	ACACCCTGGA	CAGGAACAGT	CTCTATGTCA
50351	ATGGTTTCAC	CCATCGGACC	TCTGTGCCCA	CCACCAGCAC	TCCTGGGACC
50401	TCCACAGTGG	ACCTTGGAAC	CTCAGGGACT	CCATTCTCCC	TCCAAGCCC
50451	CGCAACTGCT	GGCCCTCTCC	TGGTGCTGTT	CACCCTCAAC	TTCACCATCA
50501	CCAACCTGAA	GTATGAGGAG	GACATGCATC	GCCCTGGCTC	CAGGAAGTTC
50551	AACACCACTG	AGAGGGTCCT	GCAGACTCTG	CTTGGTCCTA	TGTTCAAGAA
50601	CACCAGTGTT	GGCCTTCTGT	ACTCTGGCTG	CAGACTGACC	TTGCTCAGGT
50651	CCGAGAAGGA	TGGAGCAGCC	ACTGGAGTGG	ATGCCA TCTG	CACCCACCGT
50701	CTTGACCCCA	AAAGCCCTGG	ACTGNACAGN	GAGCNGCTNT	ACTGGGAGCT
50751	NAGCCANCTG	ACCAANNNCA	TCNNNGAGCT	GGNCCCTAC	ACCCTGGACA
50801	GGNACAGTCT	CTATGTCAAT	GGTTTCACCC	ATCNGANCTC	TGNGCCCAACC
50851	ACCAGCACTC	CTGGGACCTC	CACAGTGNAC	NTNGGNACCT	CNNGGACTCC
50901	ATCCTCCNTC	CCNCGCCNCA	CANCNNCTGN	CCCTCTCCTG	NTNCCNTTCA
50951	CCNTCAACTT	NACCATCACC	AACCTGCANT	ANGNGGANNA	CATGCNNCNC
51001	CCNGGNTCCA	GGAAGTTCAA	CACCACNGAG	AGAGTCCTTC	AGGGTCTGCT
51051	CAGGCCTGTG	TTCAAGAACA	CCAGTGTTGG	CCCTCTGTAC	TCTGGCTGCA
51101	GACTGACCTT	GCTCAGGCCC	AAGAAGGATG	GGGCAGCCAC	CAAAGTGGAT
51151	GCCATCTGCA	CCTACCGCCC	TGATCCCAAA	AGCCCTGGAC	TGGACAGAGA
51201	GCAGCTATAC	TGGGAGCTGA	GCCAGCTAAC	CCACAGCATC	ACTGAGCTGG

Table 4 (continued)

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**Human cDNA of CA125**  
(SEQ ID NO: 4)

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51251	GCCCCTACAC	CCAGGACAGG	GACAGTCTCT	ATGTCAATGG	CTTCACCCAT
51301	CGGAGCTCTG	TGCCAACCAC	CAGTATTCCT	GGGACCTCTG	CAGTGCACCT
51351	GGAAACCACT	GGGACTCCAT	CCTCCTTCCC	CGGCCACACA	GAGCCTGGCC
51401	CTCTCCTGAT	ACCATTCACT	TTCAACTTTA	CCATCACCAA	CCTGCGTTAT
51451	GAGGAAAACA	TGCAACACCC	TGGTTCCAGG	AAGTTCAACA	CCACGGAGAG
51501	GGTTCTGCAG	GGTCTGCTCA	CGCCCTTGTT	CAAGAACACC	AGTGTGGGCC
51551	CTCTGTACTC	TGGCTGCAGA	CTGACCTTGC	TCAGACCTGA	GAAGCAGGAG
51601	GCAGCCACTG	GAGTGGACAC	CATCTGTACC	CACCGCGTTG	ATCCCATCGG
51651	ACCTGGACTG	GACAGAGAGC	GGCTATACTG	GGAGCTGAGC	CAGCTGACCA
51701	ACAGCATCAC	AGAGCTGGGA	CCCTACACCC	TGGATAGGGA	CAGTCTCTAT
51751	GTCGATGGCT	TCAACCCTTG	GAGCTCTGTG	CCAACCACCA	GCACTCCTGG
51801	GACCTCCACA	GTGCACCTGG	CAACCTCTGG	GACTCCATCC	CCCCTGCCTG
51851	GCCACACAGC	CCCTGTCCCT	CTCTTGATAC	CATTCACCCT	CAACTTTACC
51901	ATCACCGACC	TGCATTATGA	AGAAAACATG	CAACACCCTG	GTTCCAGGAA
51951	GTTCAACACC	ACGGAGAGGG	TTCTGCAGGG	TCTGCTCAAG	CCCTTGTTCA
52001	AGAGCACCAG	CGTTGGCCCT	CTGTACTCTG	GCTGCAGACT	GACCTTGCTC
52051	AGACCTGAGA	AACATGGGGC	AGCCACTGGA	GTGGACGCCA	TCTGCACCCCT
52101	CCGCCTTGAT	CCCACTGGTC	CTGGACTGGA	CAGAGAGCGG	CTATACTGGG
52151	AGCTGAGCCA	GCTGACCAAC	AGCATCACAG	AGCTGGGACC	CTACACCCTG
52201	GATAGGGACA	GTCTCTATGT	CAATGGCTTC	AACCCTTGGA	GCTCTGTGCC
52251	AACCACCAGC	ACTCCTGGGA	CCTCCACAGT	GCACCTGGCA	ACCTCTGGGA
52301	CTCCATCCTC	CCTGCCTGGC	CACACAAC TG	CTGGCCCTCT	CCTGGTGCCG
52351	TTCACCCTCA	ACTTCACCAT	CACCAACCTG	AAGTACGAGG	AGGACATGCA
52401	TTGCCCTGGC	TCCAGGAAGT	TCAACACCAC	AGAGAGAGTC	CTGCAGAGTC
52451	TGCATGGTCC	CATGTTCAAG	AACACCAGTG	TTGGCCCTCT	GTA CTCTGGC

Table 4 (continued)

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**Human cDNA of CA125**  
(SEQ ID NO: 4)

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52501	TGCAGACTGA	CCTTGCTCAG	GTCCGAGAAG	GATGGAGCAG	CCACTGGAGT
52551	GGATGCCATC	TGCACCCACC	GTCTTGACCC	CAAAAGCCCT	GGACTGNACA
52601	GNGAGCNGCT	NTACTGGGAG	CTNAGCCANC	TGACCAANNN	CATCNNNGAG
52651	CTGGGNCCCT	ACACCCTGGA	CAGGNACAGT	CTCTATGTCA	ATGGTTTCAC
52701	CCATCNGANC	TCTGNGCCCA	CCACCAGCAC	TCCTGGGACC	TCCACAGTGN
52751	ACNTNGGNAC	CTCNGGGACT	CCATCCTCCN	TCCCCNGCCN	CACANCNNCT
52801	GNCCCTCTCC	TGNTNCCNTT	CACCNTCAAC	TTNACCATCA	CCAACCTGCA
52851	NTANGNGGAN	NACATGCNNC	NCCCNGGNTC	CAGGAAGTTC	AACACCACNG
52901	AGNGNGTNCT	GCAGGGTCTG	CTNNNNCCCN	TNTTCAAGAA	CNCCAGTGTN
52951	GGCNTCTGT	ACTCTGGCTG	CAGACTGACC	TNNCTCAGGN	CNGAGAAGNA
53001	TGGNGCAGCC	ACTGGANTGG	ATGCCATCTG	CANCCACCNN	CNTNANCCCA
53051	AAAGNCCTGG	ACTGNACAGN	GAGCNGCTNT	ACTGGGAGCT	NAGCCANCTG
53101	ACCAACAGCA	TCACAGAGCT	GGGACCCCTAC	ACCCTGGATA	GGGACAGTCT
53151	CTATGTCAAT	GGTTTCACCC	ATCGAAGCTC	TATGCCCACC	ACCAGTATTC
53201	CTGGGACCTC	TGCAGTGCAC	CTGGAACCT	CTGGGACTCC	AGCCTCCCTC
53251	CCTGGCCACA	CAGCCCCTGG	CCCTCTCCTG	GTGCCATTCA	CCCTCAACTT
53301	CACTATCACC	AACCTGCAGT	ATGAGGAGGA	CATGCGTCAC	CCTGGTTCCA
53351	GGAAGTTCAA	CACCACGGAG	AGAGTCCTGC	AGGGTCTGCT	CAAGCCCTTG
53401	TTCAAGAGCA	CCAGTGTTGG	CCCTCTGTAC	TCTGGCTGCA	GACTGACCTT
53451	GCTCAGGCCT	GAAAAACGTG	GGGCAGCCAC	CGGCGTGGAC	ACCATCTGCA
53501	CTCACCGCCT	TGACCCTCTA	AACCCTGGAC	TGNACAGNGA	GCNGCTNTAC
53551	TGGGAGCTNA	GCCANCTGAC	CAANNNCATC	NNNGAGCTGG	GNCCCTACAC
53601	CCTGGACAGG	NACAGTCTCT	ATGTCAATGG	TTTACCCAT	CNGANCTCTG
53651	NGCCCACCAC	CAGCACTCCT	GGGACCTCCA	CAGTGNACNT	NGGNACCTCN
53701	GGGACTCCAT	CCTCCNTCCC	CNGCCNCACA	NCNNCTGNCC	CTCTCCTGNT

Table 4 (continued)

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 Human cDNA of CA125  
 (SEQ ID NO: 4)
 

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53751 NCCNTTCACC NTCAACTTNA CCATCACCAA CCTGCANTAN GNGGANNACA  
 53801 TGCNNCNCNC NGGNTCCAGG AAGTTCAACA CCACNGAGNG NGTNCTGCAG  
 53851 GGTCTGCTNN NCCCCNTNTT CAAGAACNCC AGTGTNGGCC NTCTGTACTC  
 53901 TGGCTGCAGA CTGACCTNNC TCAGGNCNGA GAAGNATGGN GCAGCCACTG  
 53951 GANTGGATGC CATCTGCANC CACCNNCNTN ANCCCAAAG NCCTGGACTG  
 54001 NACAGNGAGC NGCTNTACTG GGAGCTNAGC CANCTGACCA ANNNCATCNN  
 54051 NGAGCTGGGN CCCTACACCC TGGACAGGNA CAGTCTCTAT GTCAATGGTT  
 54101 TTCACCCTCG GAGCTCTGTG CCAACCACCA GCACTCCTGG GACCTCCACA  
 54151 GTGCACCTGG CAACCTCTGG GACTCCATCC TCCCTGCCTG GCCACACAGC  
 54201 CCCTGTCCCT CTCTTGATAC CATTACCCCT CAACTTTACC ATCACCAACC  
 54251 TGCATTATGA AGAAAACATG CAACACCCTG GTTCCAGGAA GTTCAACACC  
 54301 ACGGAGCGGG TCCTGCAGGG TCTGCTTGGT CCCATGTTCA AGAACACAAG  
 54351 TGTGGGCTT CTGTACTCTG GCTGCAGACT GACCTTGCTC AGGCCTGAGA  
 54401 AGAATGGGGC AGCCACTGGA ATGGATGCCA TCTGCAGCCA CCGTCTTGAC  
 54451 CCCAAAAGCC CTGGACTGNA CAGNGAGCNG CTNTACTGGG AGCTNAGCCA  
 54501 NCTGACCAAN NNCATCMNNG AGCTGGGNCC CTACACCCTG GACAGGNACA  
 54551 GTCTCTATGT CAATGGTTTC ACCCATCNGA NCTCTGNGCC CACCACCAGC  
 54601 ACTCCTGGGA CCTCCACAGT GNACNTNGGN ACCTCNGGGA CTCCATCCTC  
 54651 CNTCCCCNGC CNCACANCNN CTGNCCCTCT CCTGNTNCCN TTCACCNCA  
 54701 ACTTNACCAT CACCAACCTG CANTANGNGG ANNACATGCN NCNCCCNGGN  
 54751 TCCAGGAAGT TCAACACCAC NGAGNGNGTN CTGCAGGGTC TGCTNNNNCC  
 54801 CNTNTTCAAG AACNCCAGTG TNGGCCNTCT GTACTCTGGC TGCAGACTGA  
 54851 CCTNNCTCAG GNCNGAGAAG NATGGNGCAG CCACTGGANT GGATGCCATC  
 54901 TGCANCCACC NNCNTNANCC CAAAAGNCCT GGACTGNACA GNGAGCNGCT  
 54951 NTA CTGGGAG CTNAGCCANC TGACCAANNN CATCNNNGAG CTGGGNCCT

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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55001	ACACCCTGGA	CAGGNACAGT	CTCTATGTCA	ATGGTTTCAC	CCATCAGAAC
55051	TCTGTGCCCA	CCACCAGTAC	TCCTGGGACC	TCCACAGTGT	ACTGGGCAAC
55101	CACTGGGACT	CCATCCTCCT	TCCCCGGCCA	CACAGAGCCT	GGCCCTCTCC
55151	TGATAACATT	CACTTTCAAC	TTTACCATCA	CCAACCTGCA	TTATGAGGAA
55201	AACATGCAAC	ACCCTGGTTC	CAGGAAGTTC	AACACCACGG	AGAGGGTTCT
55251	GCAGGGTCTG	CTCACGCCCT	TGTTCAAGAA	CACCAGTGTT	GGCCCTCTGT
55301	ACTCTGGCTG	CAGACTGACC	TTGCTCAGAC	CTGAGAAGCA	GGAGGCAGCC
55351	ACTGGAGTGG	ACACCATCTG	TACCCACCGC	GTTGATCCCA	TCGGACCTGG
55401	ACTGNACAGN	GAGCNGCTNT	ACTGGGAGCT	NAGCCANCTG	ACCAANNNCA
55451	TCNNGAGCT	GGNCCCCTAC	ACCCTGGACA	GGNACAGTCT	CTATGTCAAT
55501	GGTTTCACCC	ATCNGANCTC	TGNGCCCACC	ACCAGCACTC	CTGGGACCTC
55551	CACAGTGNAC	NTNGGNACCT	CNGGGACTCC	ATCCTCCNTC	CCCNGCCNCA
55601	CANCNNCTGN	CCCTCTCCTG	NTNCCNTTCA	CCNTCAACTT	NACCATCACC
55651	AACCTGCANT	ANGNGGANNA	CATGCNNCNC	CCNGGNTCCA	GGAAGTTCAA
55701	CACCACNGAG	NGNGTNCTGC	AGGGTCTGCT	NNNNCCCNTN	TTCAAGAACN
55751	CCAGTGTTGG	CCNTCTGTAC	TCTGGCTGCA	GACTGACCTN	NCTCAGGNCN
55801	GAGAAGNATG	GNGCAGCCAC	TGGANTGGAT	GCCATCTGCA	NCCACCNNCN
55851	TNANCCCAA	AGNCCTGGAC	TGNACAGNGA	GCNGCTNTAC	TGGGAGCTNA
55901	GCCANCTGAC	CAANNNCATC	NNNGAGCTGG	GNCCCTACAC	CCTGGACAGG
55951	NACAGTCTCT	ATGTCAATGG	TTTCACCCAT	CGGAGCTCTG	TGCCAACCAC
56001	CAGCAGTCCT	GGGACCTCCA	CAGTGCACCT	GGCAACCTCT	GGGACTCCAT
56051	CCTCCCTGCC	TGGCCACACA	GCCCCTGTCC	CTCTCTTGAT	ACCATTCACC
56101	CTCAACTTTA	CCATCACCAA	CCTGCATTAT	GAAGAAAACA	TGCAACACCC
56151	TGGTTCCAGG	AAGTTCAACA	CCACGGAGAG	GGTTCTGCAG	GGTCTGCTCA
56201	AGCCCTTGTT	CAAGAGCACC	AGTGTGGGCC	CTCTGTACTC	TGGCTGCAGA

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Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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56251	CTGACCTTGC	TCAGACCTGA	GAAACATGGG	GCAGCCACTG	GAGTGGACGC
56301	CATCTGCACC	CTCCGCCTTG	ATCCCACTGG	TCCTGGACTG	NACAGNGAGC
56351	NGCTNTACTG	GGAGCTNAGC	CANCTGACCA	ANNNCATCNN	NGAGCTGGGN
56401	CCCTACACCC	TGGACAGGNA	CAGTCTCTAT	GTCAATGGTT	TCACCCATCN
56451	GANCTCTGNG	CCCACCACCA	GCACTCCTGG	GACCTCCACA	GTGNACNTNG
56501	GNACCTCNGG	GACTCCATCC	TCCNTCCCN	GCCNCACANC	NNCTGNCCCT
56551	CTCCTGNTNC	CNTTCACCNT	CAACTTNACC	ATCACCAACC	TGCANTANGN
56601	GGANNACATG	CNNCNCNG	GNTCCAGGAA	GTTCAACACC	ACNGAGNGNG
56651	TNCTGCAGGG	TCTGCTNNNN	CCCNTNTTCA	AGAACNCCAG	TGTNGGCCNT
56701	CTGTACTCTG	GCTGCAGACT	GACCTNNCTC	AGGNCNGAGA	AGNATGGNGC
56751	AGCCACTGGA	NTGGATGCCA	TCTGCANCCA	CCNNCNTNAN	CCCAAAGNC
56801	CTGGACTGNA	CAGNGAGCNG	CTNTACTGGG	AGCTNAGCCA	NCTGACCAAN
56851	NNCATCNNNG	AGCTGGGNCC	CTACACCCTG	GACAGGNACA	GTCTCTATGT
56901	CAATGGTTTC	ACCCATCGGA	CCTCTGTGCC	CACCACCAGC	ACTCCTGGGA
56951	CCTCCACAGT	GCACCTGGCA	ACCTCTGGGA	CTCCATCCTC	CCTGCCTGGC
57001	CACACAGCCC	CTGTCCCTCT	CTTGATACCA	TTCACCCTCA	ACTTTACCAT
57051	CACCAACCTG	CAGTATGAGG	AGGACATGCA	TCGCCCTGGA	TCTAGGAAGT
57101	TCAACACCAC	AGAGAGGGTC	CTGCAGGGTC	TGCTTAGTCC	CATTTTCAAG
57151	AACTCCAGTG	TTGGCCCTCT	GTACTCTGGC	TGCAGACTGA	CCTCTCTCAG
57201	GCCCGAGAAG	GATGGGGCAG	CAACTGGAAT	GGATGCTGTC	TGCCTCTACC
57251	ACCCTAATCC	CAAAAGACCT	GGGCTGGACA	GAGAGCAGCT	GTA CTGCGAG
57301	CTAAGCCAGC	TGACCCACAA	CATCACTGAG	CTGGGCCCCT	ACAGCCTGGA
57351	CAGGGACAGT	CTCTATGTCA	ATGGTTTCAC	CCATCAGAAC	TCTGTGCCCCA
57401	CCACCAGTAC	TCCTGGGACC	TCCACAGTGT	ACTGGGCAAC	CACTGGGACT
57451	CCATCCTCCT	TCCCCGGCCA	CACANCNNCT	GNCCCTCTCC	TGNTNCCNTT

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Table 4 (continued)

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**Human cDNA of CA125**  
(SEQ ID NO: 4)

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57501	CACCNTCAAC	TTNACCATCA	CCAACCTGCA	NTANGNGGAN	NACATGCNNC
57551	NCCCNGGNTC	CAGGAAGTTC	AACACCACNG	AGNGNGTNCT	GCAGGGTCTG
57601	CTNNNNCCCN	TNTTCAAGAA	CNCCAGTGTN	GGCCNTCTGT	ACTCTGGCTG
57651	CAGACTGACC	TNNCTCAGGN	CNGAGAAGNA	TGGNGCAGCC	ACTGGANTGG
57701	ATGCCATCTG	CANCCACCNN	CNTNANCCCA	AAAGNCCTGG	ACTGNACAGN
57751	GAGCNGCTNT	ACTGGGAGCT	NAGCCANCTG	ACCAANNNCA	TCNNNGAGCT
57801	GGGNCCCTAC	ACCCTGGACA	GGNACAGTCT	CTATGTCAAT	GGTTTCACCC
57851	ATTGGAGCTC	TGGGCTCACC	ACCAGCACTC	CTTGGACTTC	CACAGTTGAC
57901	CTTGGAACCT	CAGGGACTCC	ATCCCCCGTC	CCCAGCCCCA	CAACTGCTGG
57951	CCCTCTCCTG	GTGCCATTCA	CCCTAAACTT	CACCATCACC	AACCTGCAGT
58001	ATGAGGAGGA	CATGCATCGC	CCTGGATCTA	GGAAGTTCAA	CGCCACAGAG
58051	AGGGTCCTGC	AGGGTCTGCT	TAGTCCCATA	TTCAAGAACA	CCAGTGTTGG
58101	CCCTCTGTAC	TCTGGCTGCA	GACTGACCTT	GCTCAGACCT	GAGAAGCAGG
58151	AGGCAGCCAC	TGGAGTGGAC	ACCATCTGTA	CCCACCGCGT	TGATCCCATC
58201	GGACCTGGAC	TGNACAGNGA	GCNGCTNTAC	TGGGAGCTNA	GCCANCTGAC
58251	CAANNNCATC	NNNGAGCTGG	GNCCCTACAC	CCTGGACAGG	NACAGTCTCT
58301	ATGTCAATGG	TTTCACCCAT	CNGANCTCTG	NGCCCACCAC	CAGCACTCCT
58351	GGGACCTCCA	CAGTGNACNT	NGGNACCTCN	GGGACTCCAT	CCTCCNTCCC
58401	CNGCCNCACA	NCNNCTGNCC	CTCTCCTGNT	NCCNTTCACC	NTCAACTTNA
58451	CCATCACCAA	CCTGCANTAN	GNGGANNACA	TGCNNCNCCC	NGGNTCCAGG
58501	AAGTTCAACA	CCACNGAGNG	NGTNCTGCAG	GGTCTGCTNN	NNCCNTNTT
58551	CAAGAACNCC	AGTGTNGGCC	NTCTGTACTC	TGGCTGCAGA	CTGACCTNNC
58601	TCAGGNCNGA	GAAGNATGGN	GCAGCCACTG	GANTGGATGC	CATCTGCANC
58651	CACCNNCNTN	ANCCCAAAAG	NCCTGGACTG	NACAGNGAGC	NGCTNTACTG
58701	GGAGCTNAGC	CANCTGACCA	ANNNCATCNN	NGAGCTGGGN	CCCTACACCC

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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58751	TGGACAGGNA	CAGTCTCTAT	GTCAATGGTT	TCACCCATCG	GAGCTTTGGG
58801	CTCACCACCA	GCACTCCTTG	GACTTCCACA	GTTGACCTTG	GAACCTCAGG
58851	GACTCCATCC	CCCGTCCCCA	GCCCCACAAC	TGCTGGCCCT	CTCCTGGTGC
58901	CATTACCCCT	AAACTTCACC	ATCACCAACC	TGCAGTATGA	GGAGGACATG
58951	CATCGCCCTG	GCTCCAGGAA	GTTCAACACC	ACGGAGAGGG	TCCTTCAGGG
59001	TCTGCTTACG	CCCTTGTTCA	GGAACACCAG	TGTCAGCTCT	CTGTACTCTG
59051	GTTGCAGACT	GACCTTGCTC	AGGCCTGAGA	AGGATGGGGC	AGCCACCAGA
59101	GTGGATGCTG	TCTGCACCCA	TCGTCCTGAC	CCCAAAGCC	CTGGACTGNA
59151	CAGNGAGCNG	CTNCTACTGGG	AGCTNAGCCA	NCTGACCAAN	NNCATCNNNG
59201	AGCTGGGNCC	CTACACCCTG	GACAGGNACA	GTCTCTATGT	CAATGGTTTC
59251	ACCCATCNGA	NCTCTGNGCC	CACCACCAGC	ACTCCTGGGA	CCTCCACAGT
59301	GNACNTNGGN	ACCTCNGGGA	CTCCATCCTC	CNTCCCCNGC	CNCACANCNN
59351	CTGNCCCTCT	CCTGNTNCCN	TTCACCNTCA	ACTTNACCAT	CACCAACCTG
59401	CANTANGNGG	ANNACATGCN	NCNCCCNGGN	TCCAGGAAGT	TCAACACCAC
59451	NGAGNGNGTN	CTGCAGGGTC	TGCTNNNNCC	CNTNTTCAAG	AACNCCAGTG
59501	TNGGCCNTCT	GTA CTCTGGC	TGCAGACTGA	CCTNNCTCAG	GNCNGAGAAG
59551	NATGGNGCAG	CCACTGGANT	GGATGCCATC	TGCANCCACC	NNCNTNANCC
59601	CAAAAGNCCT	GGACTGNACA	GNGAGCNGCT	NTACTGGGAG	CTNAGCCANC
59651	TGACCAANNN	CATCNNNGAG	CTGGGNCCCT	ACACCCTGGA	CAGGNACAGT
59701	CTCTATGTCA	ATGGTTTCAC	CCATTGGATC	CCTGTGCCCA	CCAGCAGCAC
59751	TCCTGGGACC	TCCACAGTGG	ACCTTGGGTC	AGGGACTCCA	TCCTCCCTCC
59801	CCAGCCCCAC	AACTGCTGGC	CCTCTCCTGG	TACCATTAC	CCTCAACTTC
59851	ACCATCACCA	ACCTGCAGTA	TGGGGAGGAC	ATGGGTCACC	CTGGCTCCAG
59901	GAAGTTCAAC	ACCACAGAGA	GGGTCCTGCA	GGGTCTGCTT	GGTCCCATAT
59951	TCAAGAACAC	CAGTGTTGGC	CCTCTGTACT	CTGGCTGCAG	ACTGACCTCT



Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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60001	CTCAGGTCCG	AGAAGGATGG	AGCAGCCACT	GGAGTGGATG	CCATCTGCAT
60051	CCATCATCTT	GACCCCAAAA	GCCCTGGACT	GNACAGNGAG	CNGCTNTACT
60101	GGGAGCTNAG	CCANCTGACC	AANNNCATCN	NNGAGCTGGG	NCCCTACACC
60151	CTGGACAGGN	ACAGTCTCTA	TGTCAATGGT	TTCACCCATC	NGANCTCTGN
60201	GCCCACCACC	AGCACTCCTG	GGACCTCCAC	AGTGNACNTN	GGNACCTCNG
60251	GGACTCCATC	CTCCNTCCCC	NGCCNCACAN	CNNCTGNCCC	TCTCCTGNTN
60301	CCNTTCACCN	TCAACTTNAC	CATCACCAAC	CTGCANTANG	NGGANNACAT
60351	GCNNCNCN	GGNTCCAGGA	AGTTCAACAC	CACNGAGNGN	GTNCTGCAGG
60401	GTCTGCTNNN	NCCCNTNTTC	AAGAACNCCA	GTGTNGGCCN	TCTGTACTCT
60451	GGCTGCAGAC	TGACCTNNCT	CAGGNCNGAG	AAGNATGGNG	CAGCCACTGG
60501	ANTGGATGCC	ATCTGCANCC	ACCNNCNTNA	NCCCCAAAAGN	CCTGGACTGN
60551	ACAGNGAGCN	GCTNTACTGG	GAGCTNAGCC	ANCTGACCAA	NNNCATCINN
60601	GAGCTGGGNC	CCTACACCCT	GGACAGGNAC	AGTCTCTATG	TCAATGGTTT
60651	CACCCATCAG	ACCTTTGCGC	CCAACACCAG	CACTCCTGGG	ACCTCCACAG
60701	TGGACCTTGG	GACCTCAGGG	ACTCCATCCT	CCCTCCCCAG	CCCTACATCT
60751	GCTGGCCCTC	TCCTGGTGCC	ATTCACCCTC	AACTTCACCA	TCACCAACCT
60801	GCAGTACGAG	GAGGACATGC	ATCACCAGG	CTCCAGGAAG	TTCAACACCA
60851	CGGAGCGGGT	CCTGCAGGGT	CTGCTTGGTC	CCATGTTCAA	GAACACCAGT
60901	GTCGGCCTTC	TGTACTCTGG	CTGCAGACTG	ACCTTGCTCA	GGCCTGAGAA
60951	GAATGGGGCA	GCCACCAGAG	TGGATGCTGT	CTGCACCCAT	CGTCCTGACC
61001	CCAAAAGCCC	TGGACTGNAC	AGNGAGCNGC	TNTACTGGGA	GCTNAGCCAN
61051	CTGACCAANN	NCATCINNNGA	GCTGGGNCCC	TACACCCTGG	ACAGGNACAG
61101	TCTCTATGTC	AATGGTTTCA	CCCATCNGAN	CTCTGNGCCC	ACCACCAGCA
61151	CTCCTGGGAC	CTCCACAGTG	NACNTNGGNA	CCTCNGGGAC	TCCATCCTCC
61201	NTCCCCNGCC	NCACAGCCCC	TGTCCCTCTC	TTGATACCAT	TCAECCTCAA

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Table 4 (continued)

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Human cDNA of CA125  
(SEQ ID NO: 4)

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61251	CTTTACCATC	ACCAACCTGC	ATTATGAAGA	AAACATGCAA	CACCCTGGTT
61301	CCAGGAAGTT	CAACACCACG	GAGAGGGTTC	TGCAGGGTCT	GCTCAAGCCC
61351	TTGTTCAAGA	GCACCAGCGT	TGGCCCTCTG	TACTCTGGCT	GCAGACTGAC
61401	CTTGCTCAGA	CCTGAGAAAC	ATGGGGCAGC	CACTGGAGTG	GACGCCATCT
61451	GCACCCTCCG	CCTTGATCCC	ACTGGTCCTG	GACTGGACAG	AGAGCGGCTA
61501	TACTGGGAGC	TGAGCCAGCT	GACCAACAGC	GTTACAGAGC	TGGGCCCCTA
61551	CACCCTGGAC	AGGGACAGTC	TCTATGTCAA	TGGCTTCACC	CAGCGGAGCT
61601	CTGTGCCAAC	CACCAGTATT	CCTGGGACCT	CTGCAGTGCA	CCTGGAAACC
61651	TCTGGGACTC	CAGCCTCCCT	CCCTGGCCAC	ACAGCCCCTG	GCCCTCTCCT
61701	GGTGCCATTC	ACCCTCAACT	TCACTATCAC	CAACCTGCAG	TATGAGGTGG
61751	ACATGCGTCA	CCCTGGTTCC	AGGAAGTTCA	ACACCACGGA	GAGAGTCCTG
61801	CAGGGTCTGC	TCAAGCCCTT	GTTCAAGAGC	ACCAGTGTTG	GCCCTCTGTA
61851	CTCTGGCTGC	AGACTGACCT	TGCTCAGGCC	TGAAAAACGT	GGGGCAGCCA
61901	CCGGCGTGGA	CACCATCTGC	ACTCACC GCC	TTGACCCTCT	AAACCCTGGA
61951	CTGGACAGAG	AGCAGCTATA	CTGGGAGCTG	AGCAAACCTGA	CCCGTGGCAT
62001	CATCGAGCTG	GGCCCCCTACC	TCCTGGACAG	AGGCAGTCTC	TATGTCAATG
62051	GTTTCACCCA	TCGGAACCTT	GTGCCCATCA	CCAGCACTCC	TGGGACCTCC
62101	ACAGTACACC	TAGGAACCTC	TGAAACTCCA	TCCTCCCTAC	CTAGACCCAT
62151	AGTGCCTGGC	CCTCTCCTGG	TGCCATTAC	CCTCAACTTC	ACCATCACCA
62201	ACTTGCACTA	TGAGGAGGCC	ATGCGACACC	CTGGCTCCAG	GAAGTTCAAT
62251	ACCACGGAGA	GGGTCCTACA	GGGTCTGCTC	AGGCCCTTGT	TCAAGAATAC
62301	CAGTATCGGC	CCTCTGTACT	CCAGCTGCAG	ACTGACCTTG	CTCAGGCCAG
62351	AGAAGGACAA	GGCAGCCACC	AGAGTGGATG	CCATCTGTAC	CCACCACCCT
62401	GACCCTCAAA	GCCCTGGACT	GAACAGAGAG	CAGCTGTACT	GGGAGCTGAG
62451	CCAGCTGACC	CACGGCATCA	CTGAGCTGGG	CCCCTACACC	CTGGACAGGG

Table 4 (continued)

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 Human cDNA of CA125  
 (SEQ ID NO: 4)
 

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62501	ACAGTCTCTA	TGTCGATGGT	TTCACCTCATT	GGAGCCCCAT	ACCGACCACC
62551	AGCACTCCTG	GGACCTCCAT	AGTGAACCTG	GGAACCTCTG	GGATCCCACC
62601	TTCCCTCCCT	GAAACTACAN	CNNCTGNCCC	TCTCCTGNTN	CCNTTCACCN
62651	TCAACTTNAC	CATCACCAAC	CTGCANTANG	NGGANNACAT	GCNNCNCNCCN
62701	GGNTCCAGGA	AGTTCAACAC	CACNGAGAGG	GTTCTGCAGG	GTCTGCTCAA
62751	GCCCTTGTTT	AAGAGCACCA	GTGTTGGCCC	TCTGTATTCT	GGCTGCAGAC
62801	TGACCTTGCT	CAGGCCTGAG	AAGGACGGAG	TAGCCACCAG	AGTGGACGCC
62851	ATCTGCACCC	ACCGCCCTGA	CCCCAAAATC	CCTGGGCTAG	ACAGACAGCA
62901	GCTATACTGG	GAGCTGAGCC	AGCTGACCCA	CAGCATCACT	GAGCTGGGAC
62951	CCTACACCCCT	GGATAGGGAC	AGTCTCTATG	TCAATGGTTT	CACCCAGCGG
63001	AGCTCTGTGC	CCACCACCAG	CACTCCTGGG	ACTTTCACAG	TACAGCCGGA
63051	AACCTCTGAG	ACTCCATCAT	CCCTCCCTGG	CCCCACAGCC	ACTGGCCCTG
63101	TCCTGCTGCC	ATTCACCCTC	AATTTTACCA	TCACTAACCT	GCAGTATGAG
63151	GAGGACATGC	ATCGCCCTGG	CTCCAGGAAG	TTCAACACCA	CGGAGAGGGT
63201	CCTTCAGGGT	CTGCTTATGC	CCTTGTTCAA	GAACACCAGT	GTCAGCTCTC
63251	TGTACTCTGG	TTGCAGACTG	ACCTTGCTCA	GGCCTGAGAA	GGATGGGGCA
63301	GCCACCAGAG	TGGATGCTGT	CTGCACCCAT	CGTCCTGACC	CCAAAAGCCC
63351	TGGACTGGAC	AGAGAGCGGC	TGTACTGGAA	GCTGAGCCAG	CTGACCCACG
63401	GCATCACTGA	GCTGGGCCCC	TACACCCTGG	ACAGGCACAG	TCTCTATGTC
63451	AATGGTTTCA	CCCATCAGAG	CTCTATGACG	ACCACCAGAA	CTCCTGATAC
63501	CTCCACAATG	CACCTGGCAA	CCTCGAGAAC	TCCAGCCTCC	CTGTCTGGAC
63551	CTACGACCGC	CAGCCCTCTC	CTGGTGCTAT	TCACAATTAA	CTTCACCATC
63601	ACTAACCTGC	GGTATGAGGA	GAACATGCAT	CACCCTGGCT	CTAGAAAGTT
63651	TAACACCACG	GAGAGAGTCC	TTCAGGGTCT	GCTCAGGCCT	GTGTTCAAGA
63701	ACACCAGTGT	TGGCCCTCTG	TACTCTGGCT	GCAGACTGAC	CTTGCTCAGG

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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63751	CCCAAGAAGG	ATGGGGCAGC	CACCAAAGTG	GATGCCATCT	GCACCTACCG
63801	CCCTGATCCC	AAAAGCCCTG	GACTGGACAG	AGAGCAGCTA	TACTGGGAGC
63851	TGAGCCAGCT	AACCCACAGC	ATCACTGAGC	TGGGCCCCCTA	CACCCTGGAC
63901	AGGGACAGTC	TCTATGTCAA	TGGTTTCACA	CAGCGGAGCT	CTGTGCCCAC
63951	CACTAGCATT	CCTGGGACCC	CCACAGTGGG	CCTGGGAACA	TCTGGGACTC
64001	CAGTTTCTAA	ACCTGGTCCC	TCGGCTGCCA	GCCCTCTCCT	GGTGCTATTC
64051	ACTCTCAACT	TCACCATCAC	CAACCTGCGG	TATGAGGAGA	ACATGCAGCA
64101	CCCTGGCTCC	AGGAAGTTCA	ACACCACGGA	GAGGGTCCTT	CAGGGCCTGC
64151	TCAGGTCCCT	GTTCAAGAGC	ACCACTGTTG	GCCCTCTGTA	CTCTGGCTGC
64201	AGACTGACTT	TGCTCAGGCC	TGAAAAGGAT	GGGACAGCCA	CTGGAGTGGG
64251	TGCCATCTGC	ACCCACCACC	CTGACCCCAA	AAGCCCTAGG	CTGGACAGAG
64301	AGCAGCTGTA	TTGGGAGCTG	AGCCAGCTGA	CCCACAATAT	CACTGAGCTG
64351	GGCCACTATG	CCCTGGACAA	CGACAGCCTC	TTTGTCAATG	GTTTCACTCA
64401	TCGGAGCTCT	GTGTCCACCA	CCAGCACTCC	TGGGACCCCC	ACAGTGTATC
64451	TGGGAGCATC	TAAGACTCCA	GCCTCGATAT	TTGGCCCTTC	AGCTGCCAGC
64501	CATCTCCTGA	TACTATTAC	CCTCAACTTC	ACCATCACTA	ACCTGCGGTA
64551	TGAGGAGAAC	ATGTGGCCTG	GCTCCAGGAA	GTTCAACACT	ACAGAGAGGG
64601	TCCTTCAGGG	CCTGCTAAGG	CCCTTGTTCA	AGAACACCAG	TGTTGGCCCT
64651	CTGTACTCTG	GCTCCAGGCT	GACCTTGCTC	AGGCCAGAGA	AAGATGGGGA
64701	AGCCACCGGA	GTGGATGCCA	TCTGCACCCA	CCGCCCTGAC	CCCACAGGCC
64751	CTGGGCTGGA	CAGAGAGCAG	CTGTATTTGG	AGCTGAGCCA	GCTGACCCAC
64801	AGCATCACTG	AGCTGGGCCC	CTACACACTG	GACAGGGACA	GTCTCTATGT
64851	CAATGGTTTC	ACCCATCGGA	GCTCTGTACC	CACCACCAGC	ACCGGGGTGG
64901	TCAGCGAGGA	GCCATTCA	CTGAACTTCA	CCATCAACAA	CCTGCGCTAC
64951	ATGGCGGACA	TGGGCCAACC	CGGCTCCCTC	AAGTTCAACA	TCACAGACAA

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Table 4 (continued)

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**Human cDNA of CA125**  
(SEQ ID NO: 4)

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65001	CGTCATGAAG	CACCTGCTCA	GTCCTTTGTT	CCAGAGGAGC	AGCCTGGGTG
65051	CACGGTACAC	AGGCTGCAGG	GTCATCGCAC	TAAGGTCTGT	GAAGAACGGT
65101	GCTGAGACAC	GGGTGGACCT	CCTCTGCACC	TACCTGCAGC	CCCTCAGCGG
65151	CCCAGGTCTG	CCTATCAAGC	AGGTGTTCCA	TGAGCTGAGC	CAGCAGACCC
65201	ATGGCATCAC	CCGGCTGGGC	CCCTACTCTC	TGGACAAAGA	CAGCCTCTAC
65251	CTTAACGGTT	ACAATGAACC	TGGTCTAGAT	GAGCCTCCTA	CAACTCCCAA
65301	GCCAGCCACC	ACATTCCTGC	CTCCTCTGTC	AGAAGCCACA	ACAGCCATGG
65351	GGTACCACCT	GAAGACCCTC	AACTCAACT	TCACCATCTC	CAATCTCCAG
65401	TATTCACCAG	ATATGGGCAA	GGGCTCAGCT	ACATTCAACT	CCACCGAGGG
65451	GGTCCTTCAG	CACCTGCTCA	GACCCTTGTT	CCAGAAGAGC	AGCATGGGCC
65501	CCTTCTACTT	GGGTTGCCAA	CTGATCTCCC	TCAGGCCTGA	GAAGGATGGG
65551	GCAGCCACTG	GTGTGGACAC	CACCTGCACC	TACCACCCTG	ACCCTGTGGG
65601	CCCCGGGCTG	GACATACAGC	AGCTTTACTG	GGAGCTGAGT	CAGCTGACCC
65651	ATGGTGTAC	CCAAGTGGGC	TTCTATGTCC	TGGACAGGGA	TAGCCTCTTC
65701	ATCAATGGCT	ATGCACCCCA	GAATTTATCA	ATCCGGGGCG	AGTACCAGAT
65751	AAATTTCCAC	ATTGTCAACT	GGAACCTCAG	TAATCCAGAC	CCCACATCCT
65801	CAGAGTACAT	CACCCTGCTG	AGGGACATCC	AGGACAAGGT	CACCACACTC
65851	TACAAAGGCA	GTCAACTACA	TGACACATTC	CGTTTCTGCC	TGGTCACCAA
65901	CTTGACGATG	GACTCCGTGT	TGGTCACTGT	CAAGGCATTG	TTCTCCTCCA
65951	ATTTGGACCC	CAGCCTGGTG	GAGCAAGTCT	TTCTAGATAA	GACCCTGAAT
66001	GCCTCATTC	ATTGGCTGGG	CTCCACCTAC	CAGTTGGTGG	ACATCCATGT
66051	GACAGAAATG	GAGTCATCAG	TTTATCAACC	AACAAGCAGC	TCCAGCACCC
66101	AGCACTTCTA	CCTGAATTTT	ACCATCACCA	ACCTACCATA	TTCCAGGAC
66151	AAAGCCCAGC	CAGGCACCAC	CAATTACCAG	AGGAACAAAA	GGAATATTGA
66201	GGATGCGCTC	AACCAACTCT	TCCGAAACAG	CAGCATCAAG	AGTTATTTTT

Table 4 (continued)

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**Human cDNA of CA125**  
**(SEQ ID NO: 4)**

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66251	CTGACTGTCA	AGTTTCAACA	TTCAGGTCTG	TCCCCAACAG	GCACCACACC
66301	GGGGTGGACT	CCCTGTGTAA	CTTCTCGCCA	CTGGCTCGGA	GAGTAGACAG
66351	AGTTGCCATC	TATGAGGAAT	TTCTGCGGAT	GACCCGGAAT	GGTACCCAGC
66401	TGCAGAACTT	CACCCTGGAC	AGGAGCAGTG	TCCTTGTGGA	TGGGTATTCT
66451	CCCAACAGAA	ATGAGCCCTT	AACTGGGAAT	TCTGACCTTC	CCTTCTGGGC
66501	TGTCATCCTC	ATCGGCTTGG	CAGGACTCCT	GGGACTCATC	ACATGCCTGA
66551	TCTGCGGTGT	CCTGGTGACC	ACCCGCCGGC	GGAAGAAGGA	AGGAGAATAC
66601	AACGTCCAGC	AACAGTGCCC	AGGCTACTAC	CAGTCACACC	TAGACCTGGA
66651	GGATCTGCAA	TGACTGGAAC	TTGCCGGTGC	CTGGGGTGCC	TTTCCCCCAG
66701	CCAGGGTCCA	AAGAAGCTTG	GCTGGGGCAG	AAATAAACCA	TATTGGTCGG
66751	AAAAAAAAAA	AAAAA			

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Table 5

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**Human Protein of CA125 Molecule**  
**(SEQ ID NO: 5)**

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1	MLKPSGLPGS	SSPTRSLMTG	SRSTKATPEM	DSGLTGATLS	PKTSTGAIVV
51	TEHTLPFTSP	DKTLASPTSS	VVGRTTQSLG	VMSSALPEST	SRGMTHSEQR
101	TSPSLSPQVN	GTPSRNYPAT	SMVSGLSSPR	TRTSSTEGNF	TKEASTYTLT
151	VETTSGPVTE	KYTVPTETST	TEGDSTETPW	DTRYIPVKIT	SPMKTFADST
201	ASKENAPVSM	TPAETTVTDS	HTPGRTNPSF	GTLYSSFLDL	SPKGTPNRSG
251	ETSLELILST	TGYPFSSPEP	GSAGHSRIST	SAPLSSSASV	LDNKISETSI
301	FSGQSLTSPL	SPGVPEARAS	TMPNSAIPFS	MTLSNAETSA	ERVRSTISSL
351	GTPSISTKQT	AETILTFHAF	AETMDIPSTH	IAKTLASEWL	GSPGTLGGTS
401	TSALTTTSPS	TTLVSEETNT	HHSTSGKETE	GTLNTSMTPL	ETSAPGEESE
451	MTATLVPTLG	FTTLDKIRS	PSQVSSSHPT	RELRTTGSTS	GRQSSSTAHH
501	GSSDILRATT	SSTSKASSWT	SESTAQQFSE	PQHTQWVETS	PSMKTERPPA
551	STSVAAPITT	SVPSVVGFT	TLKTSSTKGI	WLEETSADTL	IGESTAGPTT
601	HQFAVPTGIS	MTGGSSTRGS	QGTTHLLTRA	TASSETSADL	TLATNGVPVS
651	VSPAUSKTAA	GSSPPGGTKP	SYTMVSSVIP	ETSSLQSSAF	REGTSLGLTP
701	LNTRHPFSSP	EPDSAGHTKI	STSIPLLSA	SVLEDKVSAT	STFSHHKATS
751	SITTGTPEIS	TKTKPSSAVL	SSMTLSNAAT	SPERVRNATS	PLTHPSPSGE
801	ETAGSVLTLS	TSAETTDSPN	IHPTGTLTSE	SSESPSTLSL	PSVSGVKTFP
851	SSSTPSTHLF	TSGEETEETS	NPSVSQPETS	VSRVRTTLAS	TSVPTPVFPT
901	MDTWPTRSAQ	FSSSHLVSEL	RATSSTSVTN	STGSALPKIS	HLTGATMSQ
951	TNRDTFNDSA	APQSTTWPET	SPRFKTGLPS	ATTTVSTSAT	SLSATVMVSK
1001	FTSPATSSME	ATSIREPSTT	ILTTETTNBP	GSMASASTNI	PIGKGYITEG
1051	RLDTSHLPIC	TTASSETSMD	FTMAKESVSM	SVSPSQSMDA	AGSSTPGRTS
1101	QFVDTFSDDV	YHLTSREITI	PRDGTSSALT	PQMTATHPPS	PDPGSARSTW
1151	LGILSSSPSS	PTPKVTMSST	FSTQRVTISM	IMDTVETSRW	NMPNLPSTTS
1201	LTPSNIPTSG	AIGKSTLVPL	DTPSPATSLR	ASEGGLPTLS	TYPESTNTPS

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
1251	IHLGAHASSE	SPSTINLTMA	SVVKPGSYTP	LTFPSIETHI	HVSTARMAYS
1301	SGSSPEMTAP	GETNTGSTWD	PTYIITTTDP	KDTSSAQVST	PHSVRTLRTT
1351	ENHPKTESAT	PAAYSGSPKI	SSSPNLTSPA	TKAWTITDTT	EHSTQLHYTK
1401	LAEKSSGFET	QSAPGPVSVV	IPTSPTIGSS	TLELTSDVPG	EPLVLAPSEQ
1451	TTITLPMATW	LSTSLTEEMA	STDLDISSPS	SPMSTFAIFP	PMSTPSHEL
1501	KSEADTSAIR	NTDSTTLDQH	LGIRSLGRTG	DLTTVPITPL	TTTWTSVIEH
1551	STQAQDTLSA	TMSPTHVTQS	LKDQTSIPAS	ASPSHLTEVY	PELGTQGRSS
1601	SEATTFWKPS	TDTLREIET	GPTNIQSTPP	MDNTTGGSSS	SGVTLGIAHL
1651	PIGTSSPAET	STNMALERRS	STATVSMAGT	MGLLVTSAPG	RSISQSLGRV
1701	SSVLSESTTE	GVTDSKSGSS	PRLNTQGNTA	LSSSLEPSYA	EGSQMSTSIP
1751	LTSSPTTPDV	EFIGGSTFWT	KEVTTVMTSD	ISKSSARTES	SSATLMSTAL
1801	GSTENTGKEK	LRTASMDLPS	PTPSMEVTPW	ISLTLSNAPN	TTDSLDSLHG
1851	VHTSSAGTLA	TDRSLNTGVT	RASRLENGSD	TSSKSLSMGN	STHTSMTDTE
1901	KSEVSSSIHP	RPETSAPGAE	TTLTSTPGNR	AISLTLPFSS	IPVEEVISTG
1951	ITSGPDINSA	PMTHSPITPP	TIVWTSTGTI	EQSTQPLHAV	SSEKVSQVQTQ
2001	STPYVNSVAV	SASPTHENSV	SSGSSTSSPY	SSASLES LDS	TISRRNAITS
2051	WLWDLTTS LP	TTTWPSTSLS	EALSSGHSGV	SNPSSTTTEF	PLFSAASTSA
2101	AKQRNPETET	HGPQNTAAST	LNTDASSVTG	LSETPVGASI	SSEVPLPMAI
2151	TSRSDVSGLT	SESTANPSLG	TASSAGTKLT	RTISLPTSES	LVSFRMNKDP
2201	WTVSIPLGSH	PTTNTETSIP	VNSAGPPGLS	TVASDVIDTP	SDGAESIPTV
2251	SFSPSPDTEV	TTISHFPEKT	THSFRTISSL	THELTSRVTP	IPGDWMSSAM
2301	STKPTGASPS	ITLGERRTIT	SAAPTTSPIV	LTASF TETST	VSLDNETTVK
2351	TSDILDARKT	NELPSDSSSS	SDLINTSIAS	STMDVTKTAS	ISPTSISGMT
2401	ASSSPSLFSS	DRPQVPTSTT	ETNTATSPSV	SSNTYSLDGG	SNVG GTPSTL
2451	PPFTITHPVE	TSSALLAWSR	PVRTFSTMVS	TDASGENPT	SSNSVVT SVP



Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
2501	APGTWASVGS	TTDLPAMGFL	KTSPAGEAHS	LLASTIEPAT	AFTPHLSAAV
2551	VTGSSATSEA	SLLTTSSESKA	IHSSPQTPTT	PTSGANWETS	ATPESLLVVT
2601	ETSDTTLTSK	ILVTDILFS	TVSTPPSKFP	STGTLSGASF	PTLLPDTPAI
2651	PLTATEPTSS	LATSFDSTPL	VTIASDSLGT	VPETTLTMSE	TSNGDALVLK
2701	TVSNPDRSIP	GITIQGVTES	PLHPSSTSPS	KIVAPRNTTY	EGSITVALST
2751	LPAGTTGSLV	FSQSSENSET	TALVDSSAGL	ERASVMPLTT	GSQGMASGG
2801	IRSGSTHSTG	TKTFSSLPLT	MNPGEVTAMS	EITTNRLTAT	QSTAPKGIPV
2851	KPTSAESGLL	TPVSASSSPS	KAFASLTAP	PSTWGIPQST	LTFEFSEVPS
2901	LDTKSASLPT	PGQSLNTIPD	SDASTASSSL	SKSPEKNPRA	RMMTSTKAIS
2951	ASSFQSTGFT	ETPEGSASPS	MAGHEPRVPT	SGTGDPRIAS	ESMSYPDPK
3001	ASSAMTSTSL	ASKLTTLFST	GQAARSGSSS	SPISLSTEKE	TSFLSPTAST
3051	SRKTSLFLGP	SMARQPNILV	HLQTSALTLS	PTSTLNMSQE	EPPELTSSQT
3101	IAEEEGTTAE	TQTLTFTPSE	TPTSLLEPVSS	PTEPTARRKS	SPETWASSIS
3151	VPAKTSLVET	TDGTLVTTIK	MSSQAAQNS	TWPAPAEETG	TSPAGTSPGS
3201	PEVSTTLKIM	SSKEPSISPE	IRSTVRNSPA	KTPETIVPME	TTVEPVTLOS
3251	TALGSGSTSI	SHLPTGTTSP	TKSPTENMLA	TERVSLSPSP	PEAWTNLYSG
3301	TPGGTRQSLA	TMSSVSLESP	TARSITGTGQ	QSSPELVSKT	TGMEFSMWHG
3351	STGGTTGDTH	VSLSTSSNIL	EDPVTSPNSV	SSLTDKSKHK	TETWVSTTAI
3401	PSTVLNNKIM	AAEQQTSRSV	DEAYSSSTSSW	SDQTSGSDIT	LGASPDVTNT
3451	LYITSTAQTT	SLVSLPSGDQ	GITSLTNPSG	GKTSSASSVT	SPSIGLETLR
3501	ANVSAVKSDI	APTAGHLSQT	SSPAEVSILD	VTTAPTGIS	TTITTMGTNS
3551	ISTTTPNPEV	GMSTMDSTPA	TERRTTSTEH	PSTWSSTAAS	DSWTVTDMTS
3601	NLKVARSPGT	ISTMHTTSFL	ASSTELDSMS	TPHGRITVIG	TSLVTPSSDA
3651	SAVKTETSTS	ERTLSPSDTT	ASTPISTFSR	VQRMSISVPD	ILSTSWTPSS
3701	TEAEDVPVSM	VPTDHASTKT	DPNTPLSTFL	FDSLSTLDWD	TGRSLSSATA

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
3751	TTSAPQGATT	PQELTLETMI	SPATSQLPFS	IGHITSAVTP	AAMARSSGVT
3801	FSRPDPTSKK	AEQTSTQLPT	TTSAHPGQVP	RSAATTLDDVI	PHTAKTPDAT
3851	FQRQGQTALT	TEARATSDSW	NEKEKSTPSA	PWITEMMNSV	SEDTIKEVTS
3901	SSSVLKDPEY	AGHKLGIWDD	FIPKFGKAAH	MRELPLLSP	QDKEAIHPST
3951	NTVETTGWVT	SSEHASHSTI	PAHSASSKLT	SPVTTTSTRE	QAIVSMSTTT
4001	WPESTRARTE	PNSFLTIELR	DVSPYMDTSS	TTQTSIISSP	GSTAITKGHR
4051	TEITSYKRIS	SSFLAQSMRS	SDSPSEAITR	LSNFPAMTES	GGMILAMQTS
4101	PPGATSISAP	TLDTSATASW	TGTPLATTQR	FTYSEKTTLF	SKGREDTSQP
4151	SPPCVEETSS	SSSVVPIHAT	TSPSNILLTS	QGHSPSSTPP	VTSVFLSETS
4201	GLGKTTDMSR	ISLEPGTSLP	PNLSSTAGEA	LSTYEASRDT	KAIHHSADTA
4251	VINMEATSSE	YSPIPGHTKP	SKATSPLVTS	HIMGDITSST	SVFGSSETTE
4301	IETVSSVNQG	LQERSTSQVA	SSATETSTVI	THVSSGDATT	HVTKTQATFS
4351	SGTSSISPHQ	FITSTNTFTD	VSTNPSTSLI	MTESSGVTIT	TQTGPTGAAT
4401	QGPYLLDTST	MPYLTETPLA	VTPDFMQSEK	TTLISKGPKD	VTWTSPPSVA
4451	ETSYPSLTP	FLVTTIPPAT	STLQGQHTSS	PVSATSVLTS	GLVKTDMNLN
4501	TSMEPVTNSP	QNLNNPSNEI	LATLAATTDI	ETIHPSINKA	VTNMGTASSA
4551	HVLHSTLPVS	SEPSTATSPM	VPASSMGDAL	ASISIPGSET	TDIEGEPTSS
4601	LTAGRKENST	LQEMNSTTES	NIILSNVSVG	AITEATKMEV	PSFDFATFIPT
4651	PAQSTKFPDI	FSVASSRLSN	SPPMTISTHM	TTTQTGSSGA	TSKIPLALDT
4701	STLETSAGTP	SVVTEGFAHS	KITTAMNDV	KDVSQTNPPF	QDEASSPSSQ
4751	APVLVTTLPS	SVAFTPWHS	TSSPVMSSV	LTSSLVKTAG	KVDTSLLETVT
4801	SSPQMSNTL	DDISVTSAA	TDIETHPSI	NTVVTVNGTT	GSFESHSTV
4851	SAYPEPSKVT	SPNVTTSTME	DTTISRSIPK	SSKTTRTETE	TTSSLTPKLR
4901	ETSIQEIIS	STETSTVPYK	ELTGATTEVS	RTDVTSSSS	SFPGPDQSTV
4951	SLDISTETNT	RLSTSPIMTE	SABITITTQT	GPHGATSQDT	FTMDPSNTTP

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
5001	QAGIHSAMTH	GFSQLDVTTL	MSRIPQDVSW	TSPPSVDKTS	SPSSFLSSPA
5051	MTTPSLISST	LPEDKLSSPM	TSLTSGLVK	ITDILRTRLE	PVTSSLPNFS
5101	STSDKILATS	KDSKDTKEIF	PSINTEETNV	KANNSGHESH	SPALADSETP
5151	KATTQMVITT	TVGDPAPSTS	MPVHGSSETT	NIKREPTYFL	TPRLRETSTS
5201	QESSFPTDTS	FLLSKVPTGT	ITEVSSTGVI	SSSKISTPDH	DKSTVPPDTF
5251	TGEIPRVFTS	SIKTKSAEMT	ITTQASPPES	ASHSTLPLDT	STTLSQGGTH
5301	STVSQGFYPS	EVTTLMGMP	GNVSWMTTPP	VEETSSVSSL	MSSPAMTSPS
5351	PVSSTSPQSI	PSSPLPVTL	PTSVLVTTTD	VLGTTSPESV	TSSPPNLSSI
5401	THERPATYKD	TAHTEAAMHH	STNTAVTNVG	TSGSGHKSQS	SVLADSETSK
5451	ATPLMSTAST	LGDTSVSTST	PNISQTNQIQ	TEPTASLSR	LRESSTSEKT
5501	SSTTETNTAF	SYVPTGAIQ	ASRTEISSR	TSISDLDRST	IAPDISTGMI
5551	TRLFTSPIMT	KSAEMTVTTQ	TTTPGATSQG	ILPWDSTTL	FQGGTHSTVS
5601	QGFPHSEITT	LRSRTPGDVS	WMTTPPVEET	SSGFSLMSPS	MTSPSPVSST
5651	SPESIPSSPL	PVTALLTSVL	VTTTNVLGTT	SPEPVTSSPP	NLSSPTQERL
5701	TTYKDTAHE	AMHASMTNT	AVANVGTSIS	GHEQSSVPA	DSHTSKATSP
5751	MGITFAMGDT	SVYTSTPAFF	ETRIQSESTS	SLIPGLRDTR	TSEEINTVTE
5801	TSTVLSEVPT	TTTTEVSRTE	VITSSRTTIS	GPDHSMSPY	ISTETITRLS
5851	TFPFVTGSTE	MAITNQTGPI	GTISQATLTL	DTSSASWEG	THSPVTQRFP
5901	HSEETTTMSR	STKGVSWQSP	PSVEETSSPS	SPVPLPAITS	HSSLYSAVSG
5951	SSPTSALPVT	SLTSGRRKT	IDMLDTHSEL	VTSSLPSASS	FSGEILTSEA
6001	STNTETIHFS	ENTAETNMGT	TNSMHKLHSS	VSIHSQPSGH	TPPKVTGSMM
6051	EDAIVSTSTP	GSPETKNVDR	DSTSPLTPEL	KEDSTALVMN	STTESNTVFS
6101	SVSLDAATEV	SRAEVYYDP	TFMPASAQST	KSPDISPEAS	SSHNSNPPLT
6151	ISTHKTIATQ	TGPGSVTSLG	QLTLDTSTIA	TSAGTPSART	QDFVDSETTS
6201	VMNNDLNDVL	KTSPFSAEEA	NSLSSQAPLL	VTTSPSPVTS	TLQEHSTSSL

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
6251	VSVTSVPTPT	LAKITDMDTN	LEPVTRSPQN	LRNTLATSEA	TTDTHTMHPS
6301	INTAMANVGT	TSSPNEFYFT	VSPDSDPYKA	TSVVITSTS	GDSIVSTSM
6351	RSSAMKKIES	ETTFSLIFRL	RETSTSQKIG	SSSDTSTVFD	KAFTAAATTEV
6401	SRTELTSSSR	TSIQGTEKPT	MSPDTSTRSV	TMLSTFAGLT	KSEERTIATQ
6451	TGPHRATSQG	TLTWDTSITT	SQAGTHSMT	HGFSQLDLST	LTSRVPEYIS
6501	GTSPPSVEKT	SSSSLLSLP	AITSPSPVPT	TLPESRPSSP	VHLTSLPTSG
6551	LVKTTDMLAS	VASLPPNLGS	TSHKIPTTSE	DIKDTEKMYP	STNIAVTNVG
6601	TTTSEKESYS	SVPAYSEPPK	VTSPMVTSFN	IRDTIVSTSM	PGSSEITRIE
6651	MESTFSLAHG	LKGTSTSQDP	IVSTEKSAVL	HKLTGATET	SRTEVASSRR
6701	TSIPGPDHST	ESPDISTEVI	PSLPISLGIT	ESSNMTIITR	TGPPLGSTSQ
6751	GTFTLDTPTT	SSRAGTHSMA	TQEFPHSEMT	TVMNKDPEIL	SWTIPPSIEK
6801	TSFSSSLMPS	PAMTSPPVSS	TLPKTIHTTP	SPMTSLLTPS	LVMTTDTLGT
6851	SPEPTTSSPP	NLSSTSHVIL	TTDEDTTAE	AMHPSTSTAA	TNVETTCSGH
6901	GSQSSVLTD	EKTATAPMD	TTSTMGHHTV	STMSVSSET	TKIKRESTYS
6951	LTPGLRETSI	SQNASFSTD	SIVLSEVPTG	TAEVSRTEV	TSSGRTSIPG
7001	PSQSTVLPEI	STRTMTRLFA	SPTMTESAEM	TIPTQTGPSG	STSQDTLTD
7051	TSTTKSQAKT	HSTLTQRFPH	SEMTTLMRSG	PGDMSWQSSP	SLENPSSLPS
7101	LLSLPATTSP	PPISSTLPVT	ISSSPLPVT	LLTSSPVTTT	DMLHTSPELV
7151	TSSPPKLSHT	SDERLTGKD	TTNTEAVHPS	TNTAASNVEI	PSFGHESPSS
7201	ALADSETSKA	TSPMFITSTQ	EDTTVAISTP	HFLETSRIQK	ESISLSPKL
7251	RETGSSVETS	SAIETSAVLS	EVSIGATTEI	SRTEVTSSSR	TSISGSAEST
7301	MLPEISTTRK	IIKFPTSPIL	AESSEMTIKT	QTSPPGSTSE	STFTLDTSTT
7351	PSLVITHSTM	TQRLPHSEIT	TLVSRGAGDV	PRPSSLPVEE	TSPSSQLSL
7401	SAMISPPVVS	STLPASSHSS	SASVTSPLTP	GQVKTTEVLD	ASAEPETSSP
7451	PSLSSTSVEI	LATSEVTTDT	EKIHPFPNTA	VTKVGTSSSG	HESPSSVLDP

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
7501	SETTKATSAM	GTISIMGDTs	VSTLTpALSN	TRKIQSEPAS	SLTTRLRETS
7551	TSEETSLATE	ANTVLskVST	GATTEVSRTE	AISFSRTSMS	GPEQSTMSQD
7601	ISIGTIpRIS	ASSVLTESAK	MTITTQTGPS	ESTLESTLNL	NTATTPSWVE
7651	THSIVIQGFP	HPemTTSMGR	GPGGVSWPSP	PFVKETSPPS	SPLSLPAVTS
7701	PHPVSTTFLA	HIPPSPLPVT	SLLTSGPATT	TDILGTSTEP	GTSSSSSLST
7751	TSHERLTTYK	DTAHTeAVHP	STNTGGTNVA	TTSSGYKSQS	SVLADSSPMC
7801	TTSTMGDTSV	LTSTPAFLET	RRIQTElASS	LTPGLRESSG	SEGTSsGTKM
7851	STVLskVPTG	ATTEISKEDV	TSIPGPAQST	ISPDTSTRTV	SWFSTSPVMT
7901	ESAEITMNTH	TSPLGATTQg	TSTLDTSSTT	SLTMTHSTIS	QGFSHSQMST
7951	LMRRGPEDVS	WMSPPLEKT	RPSFSLMSSP	ATTSPSPVSS	TLPEsISSSP
8001	LPVTSLLTSG	LAKTTDLHK	SSEPVTNSPA	NLSSTSVEIL	ATSEVTTDTE
8051	KTHPSSNRTV	TDVGTSSSGH	ESTSFVLADS	QTSKVTSPMV	ITSTMEDTSV
8101	STSTPGFFET	SRIQTEPTSS	LTGLRKtSS	SEGTSLATEm	STVLsgVPTG
8151	ATAEVSRTEV	TSSSRTSISG	FAQLTVSPET	STETITRLPT	SSIMTESAEM
8201	MIKTQTDPPG	STPESTHTVD	ISTTPNWVET	HSTVTQRFSH	SEMTTLVSRs
8251	PGDMLWPSQS	SVEETSSASS	LLSLPATTSP	SPVSSTLVED	FPSASLPVTS
8301	LLTPGLVITT	DRMGISREPG	TSSTSNLSST	SHERLTTLED	TVDTEAMQPS
8351	THTAVTNVRT	SISGHESQSS	VLSDSETPKA	TSSMGTTYTM	GETSVSISTS
8401	DFFETSRVQI	EPTSSLTSGL	RETSSSERIS	SATEGSTVLS	EVPSGATTEV
8451	SRTEVISSRG	TMSGPDQFT	ISPDIStEAI	TRLSTSPIMT	ESAESAITIE
8501	TGSPGATSEG	TLTLDTSSTT	FWSGTHSTAS	PGFSHSEMtt	LMSRTPGDVP
8551	WPSLPSVEEA	SSVSSSLSSP	AMTSTSFFSA	LPESISSSPH	PVTALLTLGP
8601	VKTTDMLRTS	SEPETSSPPN	LSSTSAEILA	TSEVTKDREK	IHPSSNTPVV
8651	NVGTVIYKHL	SPSSVLADLV	TTKPTSPMAT	TSTLGNTSVS	TSTPAFPETM
8701	MTQPTSSLTS	GLREISTSQE	TSSATERSAS	LSGMPTGATT	KVSrTEALSL

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
8751	GRTSTPGPAQ	STISPEISTE	TITRISTPLT	TTGSAEMTIT	PKTGHSGASS
8801	QGTFTLDTSS	RASWPGTHSA	ATHRSPHSGM	TTPMSRGPED	VSWPSRPSVE
8851	KTSPSSLVS	LSAVTSPSPL	YSTPSESSH	SPLRVTSFLT	PVMMKTTDML
8901	DTSLEPVTTT	PPSMNITSDE	SLATSKATME	TEAIQLSENT	AVTQMGITSA
8951	RQEFYSSYPG	LPEPSKVTSP	VVTSSTIKDI	VSTTIPASSE	ITRIEMESTS
9001	TLTPTPRETS	TSQEIHSATK	PSTVPYKALT	SATIEDSMTQ	VMSSSRGPSP
9051	DQSTMSQDIS	TEVITRLSTS	PIKAESTEMT	ITTQTGSPGA	TSRGTLTLDT
9101	STTFMSGTHS	TASQGFHSQ	MTALMSRTPG	DVPWLHPSV	EEASSASFSL
9151	SSPVMTSSSP	VSSTLPDSIH	SSSLPVTSL	TSGLVKTTTEL	LGTSSEPETS
9201	SPPNLSSTSA	EILATTEVTT	DTEKLEMTNV	VTSGYTHESP	SSVLADSVTT
9251	KATSSMGITY	PTGDTNVLTS	TPAFSDTSRI	QTKSKLSLTP	GLMETSISEE
9301	TSSATEKSTV	LSSVPTGATT	EVSRTAIAIS	SRTSIPGPAQ	STMSSDTSME
9351	TITRISTPLT	RKESTDMAIT	PKTGPSGATS	QGTFTLDSSS	TASWPGTHSA
9401	TTQRFQSVV	TTPMSRGPED	VSWPSPLSVE	KNSPPSSLVS	SSSVTSPSPL
9451	YSTPSGSSH	SPVPVTSFLT	SIMMKATDML	DASLEPETTS	APNMNITSDE
9501	SLATSKATTE	TEAIHVFENT	AASHVETTS	TEELYSSSPG	FSEPTKVISP
9551	VVTSSSIRDN	MVSTTMPGSS	GITRIEIESM	SSLTPGLRET	RTSQDITSST
9601	ETSTVLYKMS	SGATPEVSRT	EVMPSSRTSI	PGPAQSTMSL	DISDEVVTRL
9651	STSPIMTESA	EITITTQTGY	SLATSQVTLP	LGTSMTFLSG	THSTMSQGLS
9701	HSEMTNLMSR	GPESLSWTSP	RFVETTRSSS	SLTSLPLTTS	LSPVSSTLLD
9751	SSPSSPLPVT	SLILPGLVKT	TEVLDTSSEP	KTSSSPNLSS	TSVEIPATSE
9801	IMTDTEKIHP	SSNTAVAKVR	TSSSVHESHS	SVLADSETTI	TIPSMGITSA
9851	VDDTTVFTSN	PAFSETRRIP	TEPTFSLTPG	FRETSTSEET	TSITETSAVL
9901	YGVPTSATTE	VSMTEIMSSN	RTHIPDSDQS	TMSPDIIITEV	ITRLSSSSMM
9951	SESTQMTITT	QKSSPGATAQ	STLTLATTTA	PLARTHSTVP	PRFLHSEMTT

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)				
10001	LMSRSPENPS	WKSSPFVEKT	SSSSLLSLP	VTTSPSVSST LPQSIPSSSF
10051	SVTSLLTPGM	VKTDTSTEP	GTSLSPNLSG	TSVEILAASE VTTDTEKIHP
10101	SSSMAVTNVG	TTSSGHELYS	SVSIHSEPSK	ATYPVGTPSS MAETSISTSM
10151	PANFETTGF	AEPFSLTSG	FRKTNMSLDT	SSVTPTNTPS SPGSTHLLQS
10201	SKTDFETSSAK	TSSPDWPPAS	QYTEIPVDII	TPFNASPSIT ESTGITSFPE
10251	SRFTMSVTES	THHLSTDLLP	SAETISTGTV	MPSLSEAMTS FATTGVPRAI
10301	SGSGSPFSRT	ESGPGDATLS	TIAESLPSS	PVPFSSSTFT TDSSTIPAL
10351	HEITSSSATP	YRVDTSLGTE	SSTTEGRLVM	VSTLDTSSQP GRTSSTPILD
10401	TRMTESVELG	TVTSAYQVPS	LSTRLLTRTDG	IMEHITKIPN EAAHRTIRP
10451	VKGPQTSTSP	ASPKGLHTGG	TKRMETTTTA	LKTTTTALKT TSRATLTTSV
10501	YTPTLGLTLP	LNASRQMAST	ILTEMMITTP	YVFPDVPETT SSLATSLGAE
10551	TSTALPRTTP	SVLNRESETT	ASLVSRSGAE	RSPVIQTLDV SSSEPDTTAS
10601	WVIHPAETIP	TVSKTTPNFF	HSELDTVSST	ATSHGADVSS AIPTNISPSE
10651	LDALTPLVTI	SGTDTSTTFP	TLTKSPHETE	TRTTWLTHPA ETSSTIPRTI
10701	PNFSHHESDA	TPSIATSPGA	ETSSAIPIMT	VSPGAEDLVT SQVTSSGTDR
10751	NMTIPTLTLS	PGEPKTIASL	VTHPEAQTS	AIPTSTISPA VSRLVTSMT
10801	SLAAKTSTTN	RALTNSPGEP	ATTVSLVTHP	AQTSPTVPWT TSIFFHKS
10851	TTPSMTTSHG	AESSAVPTP	TVSTEVPGVV	TPLVTSSRAV ISTTIPILTL
10901	SPGEPETTPS	MATSHGEEAS	SAIPTPTVSP	GVPGVVTSLV TSSRAVTSTT
10951	IPILTFSLGE	PETTPSMATS	HGTEAGSAVP	TVLPEVPGMV TSLVASSRAV
11001	TSTTLPTLTL	SPGEPETTPS	MATSHGAEAS	STVPTVSPEV PGVVTSLVTS
11051	SSGVNSTSIP	TLILSPGELE	TTPSMATSHG	AEASSAVPTP TVSPGVSGVV
11101	TPLVTSSRAV	TSTTIPILTL	SSSEPETTPS	MATSHGVEAS SAVLTVSPEV
11151	PGMVTSLVTS	SRAVTSTTIP	TLTSSDEPE	TTTSLVTHSE AKMISAIPTL
11201	AVSPTVQGLV	TSLVTSSGSE	TSAFSNLTVA	SSQPETIDSW VAHPGTEASS

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
11251	VVPTLTVSTG	EPFTNISLVT	HPAESSSTLP	RTTSRFSHSE	LDTMPSTVTS
11301	PEAESSSAIS	TTISPGIPGV	LTSLVTSSEGR	DISATFPPTVP	ESPHESEATA
11351	SWVTHPAVTS	TTVPRITPNY	SHSEPDTTPS	IATSPGAEAT	SDFPTITVSP
11401	DVPDMVTSQV	TSSGTDTSIT	IPTLTLSSE	PETTTSFITY	SEHTTSSAIP
11451	TLPVSPGASK	MLTSLVISSG	TDSTTTFPTL	TETPYEPETT	AIQLIHPAET
11501	NTMVPRTTPK	FSHKSDDTL	PVAITSPGPE	ASSAVSTTTI	SPDMSDLVTS
11551	LVPSSGTDTS	TTFPTLSETP	YEPETTATWL	THPAETSTTV	SGTIPNFSHR
11601	GSDTAPSMVT	SPGVDTRSGV	PTTIPPSIP	GVVTSQVTSS	ATDTSTAAPT
11651	LTPSPGEPET	TASSATHPGT	QTGFTVPIRT	VPSSEPDTMA	SWVTHPPQTS
11701	TPVSRTTSSF	SHSSPDATPV	MATSPRTEAS	SAVLTTISPG	APEMVTSQIT
11751	SSGAATSTTV	PTLTHSPGMP	ETTALLSTHP	RTETSKTFPA	STVFPQVSET
11801	TASLTIRPGA	ETSTALPTQT	TSSLFTLLVT	GTSRVDLSPT	ASPGVSAKTA
11851	PLSTHPGTET	STMIPTSTLS	LGLLETTGLL	ATSSSAETST	STLTTLTVSPA
11901	VSGLSSASIT	TDKPQTVTSW	NTETSPSVTS	VGPPEFSRTV	TGTTMTLIPS
11951	EMPTPPKTSH	GEGVSPTTIL	RTTMVEATNL	ATTGSSPTVA	KTTTTFNTLA
12001	GSLFTPLTTP	GMSTLASESV	TSRTSYNHR	WISTTSSYNR	RYWTPATSTP
12051	VTSTFSPGIS	TSSIPSSATA	TVPFMVPFTL	NFTITNLQYE	EDMRHPGSRK
12101	FNATERELQG	LLKPLFRNSS	LEYLYSGCRL	ASLRPEKDSS	AMAVDAICTH
12151	RPDPEDLGLD	RERLYWELSN	LTNGIQELGP	YTLDRNSLYV	NGFTHRSSMP
12201	TTSTPGTSTV	DVGTSCTPSS	SPSPTAAGPL	LMPFTLNFTI	TNLQYEEDMR
12251	RTGSRKFNTM	ESVLQGLLKP	LFKNTSVGPL	YSGCRLTLR	PEKDGAATGV
12301	DAICTHRLDP	KSPGLNREQ	YWELSKLTND	IEELGPYTLD	RNSLYVNGFT
12351	HQSSVSTTST	PGTSTVDLRT	SGTPSSLSSP	TIMAAGPLL	PFTLNFTITN
12401	LQYGEDMGHP	GSRKFNTTER	VLQGLLGPIF	KNTSVGPLY	GCRLTSLRSE
12451	KDGAATGVDA	ICIHHLDPKS	PGLNRERLYW	ELSQLTNGIK	ELGPYTLDNR



Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)							
12501	SLYVNGFTHR	TSVPTSSTPG	TSTVDLGTSG	TPFSLPSPAT	AGPLLVLFTL		
12551	NFTITNLKYE	EDMHRPGSRK	FNTTERVLQT	LLGPMFKNTS	VGLLYSGCRL		
12601	TLLRSEKDGA	ATGVDAICTH	RLDPKSPGLD	REQLYWELSQ	LTNGIKELGP		
12651	YTLDNRNSLYV	NGFTHWIPVP	TSSTPGTSTV	DLGSGTPSSL	PSPTAAGPLL		
12701	VPFTLNFTIT	NLQYEEDMHH	PGSRKFNTTE	RVLQGLLGPM	FKNTSVGLLY		
12751	SGCRLTLLRS	EKDGAATGVD	AICTHRLDPK	SPGVDREQLY	WELSQTNGI		
12801	KELGPYTLDR	NSLYVNGFTH	QTSAPNTSTP	GTSTVDLGTS	GTPSSLPSPT		
12851	SAGPLLVPFT	LNFTITNLQY	EEDMRHPSGR	KFNTTERVLQ	GLLKPLFKST		
12901	SVGPLYSGCR	LTLRSEKDG	AATGVDAICT	HRLDPKSPGV	DREQLYWELS		
12951	QLTNGIKELG	PYTLDRNSLY	VNGFTHQ TSA	PNTSTPGTST	VDLGTSGTPS		
13001	SLPSPTSAGP	LLVPFTLNFT	ITNLQYEEDM	HHPGSRKFNT	TERVLQGLLG		
13051	PMFKNTSVGL	LYSGCRLTLL	RPEKNGAATG	MDAICSHRLD	PKSPGLNREQ		
13101	LYWELSQTTH	GIKELGPYTL	DRNSLYVNGF	THRSSVAPTS	TPGTSTVDLG		
13151	TSGTPSSLPS	PTTAVPLLVP	FTLNFTITNL	QYGEDMRHPG	SRKFNTTERV		
13201	LQGLLGPLFK	NSSVGPLYSG	CRLISLRSEK	DGAATCVD AI	CTHHLNPQSP		
13251	GLDREQLYWQ	LSQMTNGIKE	LGPYTLDRNS	LYVNGFTHRS	SGLTTSTPWT		
13301	STVDLGTSGT	PSPVPSPTTA	GPLLVPFTLN	FTITNLQYEE	DMHRPGSRKF		
13351	NATERVLQGL	LSPIFKNSSV	GPLYSGCRLT	SLRPEKDGA	TGMDAVCLYH		
13401	PNPKRPGLDR	EQLYWELSQT	THNITELGPY	SLDRDSLYVN	GFTHQNSVPT		
13451	TSTPGTSTVY	WATTGTPSSF	PGHTEPGPLL	IPFTFNFTIT	NLHYEENMQH		
13501	PGSRKFNTTE	RVLQGLLKPL	FKNTSVGPLY	SGCRLTSLRP	EKDGAATGMD		
13551	AVCLYHPNPK	RPGLDREQLY	CELSQLTHNI	TELGPYSLDR	DSLYVNGFTH		
13601	QNSVPTTSTP	GTSTVYWATT	GTPSSFPGHT	EPGPLLIPFT	FNFTITNLHY		
13651	EENMQHPGSR	KFNTTERVLQ	GLLKPLFKNT	SVGPLYSGCR	LTLRPEKHE		
13701	AATGVDTICT	HRVDPIGPGL	DRERLYWELS	QLTNSITELG	PYTLDRDSLY		

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
13751	VNGFNPRSSV	PTTSTPGTST	VHLATSGTPS	SLPGHTAPVP	LLIPFTLNFT
13801	ITNLHYEENM	QHPGSRKFNT	TERVLQGLLK	PLFKNTSVGP	LYSGCRLTLL
13851	RPEKHEAATG	VDTICTHRVD	PIGPGLDREX	LYWELSXLTX	XIXELGPYXL
13901	DRXSLYVNGF	XXXXXXXXTS	TPGTSXVXLX	TSGTPXXXPX	XTSAGPLLVP
13951	FTLNFTITNL	QYEEDMHHPG	SRKFNTTERV	LQGLLGPMFK	NTSVGLLYSG
14001	CRLTLLRPEK	NGAATGMDAI	CSHRLDPKSP	GLDREQLYWE	LSQLTHGIKE
14051	LGPYTLDNRN	LYVNGFTHRS	SVAPTSTPGT	STVDLGTSQT	PSSLPSPTTA
14101	VPLLVPFTLN	FTITNLQYGE	DMRHGSRKF	NTTERVLQGL	LGPLFKNSSV
14151	GPLYSGCRLI	SLRSEKDGA	TGVDAICTHH	LNPQSPGLDR	EQLYWQLSQM
14201	TNGIKELGPY	TLDNRNLYVN	GFTHRSSGLT	TSTPWTSTVD	LGTSQTSPSV
14251	PSPTTAGPLL	VPFTLNFTIT	NLQYEEDMHR	PGSRKFNATE	RVLQGLLSPI
14301	FKNSSVGPLY	SGCRLTSLRP	EKDGAATGMD	AVCLYHPNPK	RPGLDREQLY
14351	WELSQLTHNI	TELGPYSLDR	DSLYVNGFTH	QSSMTTTRTP	DTSTMHLATS
14401	RTPASLSGPT	TASPLLVLFT	INCTITNLQY	EEDMRRTGSR	KFNTMESVLQ
14451	GLLKPLFKNT	SVGPLYSGCR	LTLRPPKDG	AATGVDAICT	HRLDPKSPGL
14501	NREQLYWELS	KLNDIEELG	PYTLDNRNLY	VNGFTHQSSV	STTSTPGTST
14551	VDLRTSGTPS	SLSSPTIMXX	XPLLXPFTLN	FTITNLXYEE	MXXPGRSRKF
14601	NTTERVLQGL	LRPLFKNTSV	SSLYSGCRLT	LLRPEKDGA	TRVDAACTYR
14651	PDPKSPGLDR	EQLYWELSQL	THSITELGPY	TLDNRNLYVN	GFNPRSSVPT
14701	TSTPGTSTVH	LATSGTPSSL	PGHTXXXPLL	XPFTLNFTIT	NLXYEEXMXX
14751	PGSRKFNTTE	RVLQGLLKPL	FRNSSLEYLY	SGCRLASLRP	EKDSSAMAVD
14801	AICTHRPDPE	DLGLDRERLY	WELSNLTNGI	QELGPYTLDNR	NLYVNGFTH
14851	RSSFLTSTP	WTSTVDLGTS	GTPSPVPSPT	TAGPLLVPFT	LNFTITNLQY
14901	EEDMRPGSR	RFNTTERVLQ	GLLTPLFKNT	SVGPLYSGCR	LTLRPEKQE
14951	AATGVDTICT	HRVDPIGPGL	DRERLYWELS	QLTNSITELG	PYTLDNRDSLY

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
15001	VNGFNPWSSV	PTTSTPGTST	VHLATSGTPS	SLPGHTAPVP	LLIPFTLNFT
15051	ITDLHYEENM	QHPGSRKFNT	TERVLQGLLK	PLFKSTSVGP	LYSGCRLTLL
15101	RPEKHGAATG	VDAICTLRLD	PTGPGLDRE	LYWELSQLTN	SVTELGPYTL
15151	DRDSLYVNGF	THRSSVPTTS	IPGTSAVHLE	TSGTPASLPG	HTAPGPPLLVP
15201	FTLNFTITNL	QYEEDMRHPG	SRKFSTTERV	LQGLLKPLFK	NTSVSSSLYSG
15251	CRLTLLRPEK	DGAATRVDV	CTHRPDPKSP	GLDRERLYWK	LSQLTHGITE
15301	LGPYTLDRHS	LYVNGFTHQS	SMTTTRTPDT	STMHLATSRT	PASLSGPTTA
15351	SPLLVLFTIN	FTITNQRYEE	NMHPGSRKF	NTTERVLQGL	LRPVFKNTSV
15401	GPLYSGCRLT	LLRPKKGAA	TKVDAICTYR	PDPKSPGLDR	EQLYWELSQL
15451	THSITELGPI	TQDRDSLYVN	GFTHRSSVPT	TSIPGTSAVH	LETSGTPASL
15501	PGHTAPGPLL	VPFTLNFTIT	NLQYEEDMRH	PGSRKFNTTE	RVLQGLLKPL
15551	FKSTSVGPLY	SGCRLTLLRP	EKRGAAATGVD	TICTHRLDPL	NPGLDREQLY
15601	WELSKLTRGI	IELGPYLLDR	GSLYVNGFTH	RTSVPTTSTP	GTSTVDLGT
15651	GTPFSLPSA	XXXPLLXPFT	LNFTITNLXY	EEXMXXPGSR	KFNTTERVLQ
15701	TLLGPMFKNT	SVGLLYSGCR	LTLRSEKDG	AATGVDAICT	HRLDPKSPGV
15751	DREQLYWELS	QLTNGIKELG	PYTLDNRSLY	VNGFTHWIPV	PTSSTPGTST
15801	VDLGSGTPSL	PSSPTTAGPL	LVPFTLNFTI	TNLKYEEDMH	CPGSRKFNTT
15851	ERVLQSLG	MPKNTSVGPI	YSGCRLTLLR	SEKDGAATGV	DAICTHRLDP
15901	KSPGVDREQL	YWELSQLTNG	IKELGPYTLD	RNSLYVNGFT	HQTSAPNTST
15951	PGTSTVDLGT	SGTPSSLPS	TXXXPLLXPF	TLNFTITNLX	YEEKMXXPGS
16001	RKFNTTERVL	QGLLXPXFKX	TSVGXLYSGC	RLTLRXEKX	XAATXVDXXC
16051	XXXXDPXXPG	LDREXLYWEL	SXLTXIXEL	GPYXLDXSL	YVNGFTHWIP
16101	VPTSSTPGTS	TVDLGSGTPS	SLPSPTTAGP	LLVPFTLNFT	ITNLKYEEDM
16151	HCPGSRKFNT	TERVLQSLG	PMFKNTSVGP	LYSGCRLTSL	RSEKDGAATG
16201	VDAICTHRVD	PKSPGVDREQ	LYWELSQLTN	GIKELGPYTL	DRNSLYVNGF

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
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16301	QYEEDMHHPG	SRKFNTTERV	LQGLLGPMFK	NTSVGLLYSG	CRLTLLRPEK
16351	NGAATGMDAI	CTHRLDPKSP	GLDREXLYWE	LSXLTXIXE	LGPYXLDKXS
16401	LYVNGFXXXX	XXXXTSTPGT	SKVXLXSGT	PXXXPXXTX	XPLLXPFTLN
16451	FTITNLXYEE	XXXXPGSRKF	NTTERVLQGL	LKPLFRNSSL	EYLYSGCRLA
16501	SLRPEKDSSA	MAVDAICTHR	PDPEGLGLDR	ERLYWELSNL	TNGIQELGPY
16551	TLDRNSLYVN	GFTHRSMPT	TSTPGTSTVD	VGTSCTPSSS	PSPTTAGPLL
16601	IPFTLNFTIT	NLQYGEDMGH	PGSRKFNTTE	RVLQGLLGPI	FKNTSVGPLY
16651	SGCRLTSLRS	EKDGAATGVD	AICIHHLDPK	SPGLNRERLY	WELSQTNGI
16701	KELGPYTLDR	NSLYVNGFTH	RTSVPTTSTP	GTSTVDLGTS	GTPFSLPSPA
16751	TAGPLLVLFT	LNFTITNLKY	EEDMHRPGSR	KFNTTERVLQ	TLLGPMFKNT
16801	SVGLLYSGCR	LTLLRSEKDG	AATGVDAICT	HRLLDPKSPGL	DREXLYWELS
16851	XLTXIXELG	PYXLDKXSLY	VNGFXXXXXX	XTSTPGTSX	VXLXSGTPX
16901	XXPXXTXXXP	LLXPFTLNFT	ITNLXYEEXM	XXPGSRKFNT	TERVLQGLLR
16951	PVFKNTSVGP	LYSGCRLTLL	RPKKDGAATK	VDAICTYRPD	PKSPGLDREQ
17001	LYWELSQTTH	SITELGPYTQ	DRDSLYVNGF	THRSSVPTTS	IPGTSVHLE
17051	TTGTPSSFPG	HTEPGPLLIP	FTFNFTITNL	RYEENMQHPG	SRKFNTTERV
17101	LQGLLTPLFK	NTSVGPLYSG	CRLTLLRPEK	QEAATGVDTI	CTHRVDPIGP
17151	GLDRERLYWE	LSQLTNSITE	LGPYTLDRDS	LYVDGFNPWS	SVPTTSTPGT
17201	STVHLATSGT	PSPLPGHTAP	VPLLIPFTLN	FTITDLHYEE	NMQHPGSRKF
17251	NTTERVLQGL	LKPLFKSTSV	GPLYSGCRLT	LLRPEKHGAA	TGVDAICTLR
17301	LDPTGPGLDR	ERLYWELSQT	TNSITELGPY	TLDRDSLYVN	GFNPWSSVPT
17351	TSTPGTSTVH	LATSGTPSSL	PGHTTAGPLL	VPFTLNFTIT	NLKYEEDMHC
17401	PGSRKFNTTE	RVLQSLHGPM	FKNTSVGPLY	SGCRLTLLRS	EKDGAATGVD
17451	AICTHRLDPK	SPGLDREXLY	WELSXLTXI	XELGPYXLDK	XSLYVNGFXX

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
17501	XXXXXXTSTP	GTSXVXLXTS	ĠTPXXXPXXT	XXXPLLXPFT	LNFTITNLXY
17551	EEXMXXPGSR	KFNTTERVLQ	GLLXPXFKXT	SVGXLYSGCR	LTLRLRXEKKX
17601	AATXVDXXCX	XXXDPXXPGL	DREXLYWELS	XLTNSITELG	PYTLDRDSLY
17651	VNGFTHRSSM	PTTSIPGTSA	VHLETSGTPA	SLPGHTAPGP	LLVPFTLNFT
17701	ITNLQYEEDM	RHPGSRKFNT	TERVLQGLLK	PLFKSTSVGP	LYSGCRLTLL
17751	RPEKRGAAATG	VDTICTHRLD	PLNPGLDREX	LYWELSXLTX	XIXELGPYXL
17801	DRXSLYVNGF	XXXXXXXXTS	TPGTSXVXLX	TSGTPXXXPX	XTXXXPLLXP
17851	FTLNFTITNL	XYEEXMXXPG	SRKFNTTERV	LQGLLXPXFK	XTSVGXLYSG
17901	CRLTLLRXEK	XXAATXVDXX	CXXXXDPXXP	GLDREXLYWE	LSXLTXIXE
17951	LGPYXLDRXS	LYVNGFHPRS	SVPTTSTPGT	STVHLATSGT	PSSLPGHTAP
18001	VPLLIPFTLN	FTITNLHYEE	NMQHPGSRKF	NTTERVLQGL	LGPMFKNTSV
18051	GLLYSGCRLT	LLRPEKNGAA	TGMDAICSHR	LDPKSPGLDR	EXLYWELSXL
18101	TXXIXELGPY	XLDRXSLYVN	GFXXXXXXXXX	TSTPGTSXVX	LXTSGTPXXX
18151	PXXTXXXPLL	XPFTLNFTIT	NLXYEEXMXX	PGSRKFNTTE	RVLQGLLXPX
18201	FKXTSVGXLY	SGCRLTLLRX	EKXXAATXVD	XXCXXXXDPX	XPGLDREXLY
18251	WELSXLTXXI	XELGPYXLDR	XSLYVNGFTH	QNSVPTTSTP	GTSTVYWATT
18301	GTPSSFPGHT	EPGPLLIPFT	FNFTITNLHY	EENMQHPGSR	KFNTTERVLQ
18351	GLLTPLFKNT	SVGPLYSGCR	LTLRLPEKQE	AATGVDTICT	HRVDPIGPGL
18401	DREXLYWELS	XLTXIXELG	PYXLDRXSLY	VNGFXXXXXX	XTSTPGTSX
18451	VXLXTSGTPX	XXPXXTXXXP	LLXPFTLNFT	ITNLXYEEXM	XXPGSRKFNT
18501	TERVLQGLLX	PXFKXTSVGX	LYSGCRLTLL	RXEKXXAATX	VDXXCXXXXD
18551	PXXPGLDREX	LYWELSXLTX	XIXELGPYXL	DRXSLYVNGF	THRSSVPTTS
18601	SPGTSTVHLA	TSGTPSSLPG	HTAPVPLLIP	FTLNFTITNL	HYEENMQHPG
18651	SRKFNTTERV	LQGLLKPLFK	STSVGPLYSG	CRLTLLRPEK	HGAATGVDAI
18701	CTLRDPTGP	GLDREXLYWE	LSXLTXIXE	LGPYXLDRXS	LYVNGFXXXX

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
18751	XXXXTSTPGT	SXVXLXTSQT	PXXXPXXTXX	XPLLXPFTLN	FTITNLXYEE
18801	XMXXPGSRKF	NTTERVLQGL	LXPXFKXTSV	GXLYSGCRLT	LLRXEKXXAA
18851	TXVDXXCXXX	XDPPXPGLDR	EXLYWELSXL	TXXIXELGPY	XLDRXSPLYVN
18901	GFTHRTSVPT	TSTPGTSTVH	LATSGTPSSL	PGHTAPVPLL	IPFTLNFTIT
18951	NLQYEEDMHR	PGSRKFNTTE	RVLQGLLSPI	FKNSSVGPLY	SGCRLTSLRP
19001	EKDGAATGMD	AVCLYHPNPK	RPGLDREQLY	CELSQLTHNI	TELGPLYSLDR
19051	DSLYVNGFTH	QNSVPTTSTP	GTSTVYWATT	GTPSSFPGHT	XXXPLLXPFT
19101	LNFTITNLXY	EEXMXXPGSR	KFNTTERVLQ	GLLXPXFKXT	SVGXLYSGCR
19151	LTLRLXKXX	AATXVDXXCX	XXXDPXXPGL	DREXLYWELS	XLTXIXELG
19201	PYXLDRXSLY	VNGFTHWSSG	LTTSTPWTST	VDLGTSGTPS	PVPSPTTAGP
19251	LLVPFTLNFT	ITNLQYEEDM	HRPGSRKFNA	TERVLQGLLS	PIFKNTSVGP
19301	LYSGCRLTLL	RPEKQEAATG	VDTICTHRVD	PIGPGLDREX	LYWELSXLTX
19351	XIXELGPYXL	DRXSPLYVNGF	XXXXXXXXXTS	TPGTSXVXLX	TSGTPXXXPX
19401	XTXXXPLLXP	FTLNFTITNL	XYEEXMXXPG	SRKFNTTERV	LQGLLXPXFK
19451	XTSVGXLYSG	CRLTLRLXKX	XXAATXVDXX	CXXXDPXXP	GLDREXLYWE
19501	LSXLTXIXE	LGPYXLDRXS	LYVNGFTHRS	FGLTTSTPWT	STVDLGTSGT
19551	PSPVPSPTTA	GPLLVPFTLN	FTITNLQYEE	DMHRPGSRKF	NTTERVLQGL
19601	LTPLFRNTSV	SSLYSGCRLT	LLRPEKDGA	TRVDAVCTHR	PDPKSPGLDR
19651	EXLYWELSXL	TXXIXELGPY	XLDRXSPLYVN	GFXXXXXXXXX	TSTPGTSXVX
19701	LXTSGTPXXX	PXXTXXXPLL	XPFTLNFTIT	NLXYEEXMXX	PGSRKFNTTE
19751	RVLQGLLXPX	FKXTSVGXLY	SGCRLTLRLX	EKXXAATXVD	XXCXXXDPX
19801	XPGLDREXLY	WELSXLTXXI	XELGPYXLDR	XSLYVNGFTH	WIPVPTSSTP
19851	GTSTVDLGSG	TPSSLPSPTT	AGPLLVPFTL	NFTITNLQYG	EDMGHPGSRK
19901	FNTTERVLQG	LLGPIFKNTS	VGPLYSGCRL	TSLRSEKDGA	ATGVDAICIH
19951	HLPKSPGLD	REXLYWELSX	LTXIXELGP	YXLDRXSPLYV	NGFXXXXXXXX

Table 5 (continued)

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**Human Protein of CA125 Molecule**  
(SEQ ID NO: 5)

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20001	XTSTPGTSXV	XLXTSGTPXX	XPXXTXXXPL	LXPFTLNFTI	TNLXYEEXMX
20051	XPGSRKFNTT	ERVLQGLLXP	XFKXTSVGXL	YSGCRLTLLR	XEKXXAATXV
20101	DXXCXXXXDP	XXPGLDREXL	YWELSXLTX	IXELGPYXLD	RXSLYVNGFT
20151	HQTFAPNTST	PGTSTVDLGT	SGTPSSLPSP	TSAGPLLVPF	TLNFTITNLQ
20201	YEEDMHHPGS	RKFNTTTERVL	QGLLGPMFKN	TSVGLLYSGC	RLTLLRPEKN
20251	GAATRVDVAVC	THRPDPKSPG	LDREXLYWEL	SXLTXIXEL	GPYXLDRXSL
20301	YVNGFXXXXX	XXXTSTPGTS	XVXLXTSGTP	XXXPXXTAPV	PLLIPFTLNF
20351	TITNLHYEEN	MQHPGSRKFN	TTERVLQGLL	RPLFKSTSVG	PLYSGCRLTL
20401	LRPEKHGAAT	GVDAICTLRL	DPTGPGLDRE	RLYWELSQLT	NSVTELGPYT
20451	LDRDSLYVNG	FTQRSSVPTT	SIPGTSAVHL	ETSGTPASLP	GHTAPGPLL
20501	PFTLNFTITN	LQYEVDMRHP	GSRKFNTTER	VLQGLLKPLF	KSTSVGPLYS
20551	GCRLTLLRPE	KRGAATGVDT	ICTHRLDPLN	PGLDREQLYW	ELSKLTRGII
20601	ELGPYLLDRG	SLYVNGFTHR	NFVPITSTPG	TSTVHLGTSE	TPSSLPRPIV
20651	PGPLLVPFTL	NFTITNLQYE	EAMRHGSRK	FNTTTERVLQ	LLRPLFKNTS
20701	IGPLYSSCRL	TLLRPEKDKA	ATRVDAICTH	HPDPQSPGLN	REQLYWELSQ
20751	LTHGITELGP	YTLDRDSLYV	DGFTHWSPIP	TTSTPGTSIV	NLGTSGIPPS
20801	LPETTXXXPL	LXPFTLNFTI	TNLXYEEXMX	XPGSRKFNTT	ERVLQGLLKP
20851	LFKSTSVGPL	YSGCRLTLLR	PEKDGVA TRV	DAICTHRPDP	KIPGLDRQQL
20901	YWELSQLTHS	ITELGPYTLD	RDSLYVNGFT	QRSSVPTTST	PGTFTVQPET
20951	SETPSSLPGP	TATGPVLLPF	TLNFTITNLQ	YEEDMHRPGS	RKFNTTTERVL
21001	QGLLMPLFKN	TSVSSLYSGC	RLTLLRPEKD	GAATRVDVAVC	THRPDPKSPG
21051	LDRERLYWKL	SQLTHGITEL	GPYTLDRHSL	YVNGFTHQSS	MTTTRTPDTS
21101	TMHLATS RTP	ASLSGPTTAS	PLLVLF TINF	TITNLRYEEN	MHHPGSRKFN
21151	TTERVLQGLL	RPVFKNTSVG	PLYSGCRLTL	LRPKKDGAAT	KVDAICTYRP
21201	DPKSPGLDRE	QLYWELSQLT	HSITELGPYT	QDRDSLYNNG	FTQRSSVPTT

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
21251	SVPGTPTVDL	GTSGTPVSKP	GPSAASPLLV	LFTLNGTITN	LRYEENMQHP
21301	GSRKFNTTER	VLQGLLRSLF	KSTSVGPLYS	GCRLTLLRPE	KDGTATGVDA
21351	ICTHHPDPKS	PRLDREQLYW	ELSQLTHNIT	ELGHYALDND	SLFVNGFTHR
21401	SSVSTTSTPG	TPTVYLGAASK	TPASIFGPSA	ASHLLILFTL	NFTITNLRYE
21451	ENMWPGSRKF	NTTERVLQGL	LRPLFKNTSV	GPLYSGSRLT	LLRPEKDGEA
21501	TGVDAICTHR	PDPTGPGLDR	EQLYLELSQL	THSITELGPY	TLDRDSLIVN
21551	GFTHRSSVPT	TSTGVVSEEP	FTLNFTINNL	RYMADMGQPG	SLKFNITDNV
21601	MKHLLSPLFQ	RSSLGARYTG	CRVIALRSVK	NGAETRVDLL	CTYLQPLSGP
21651	GLPIKQVFHE	LSQQTHGITR	LGPYSLDKDS	LYLNGYNEPG	LDEPPTTPKP
21701	ATTFLPPLSE	ATTAMGYHLK	TLTLNFTISN	LQYSPDMGKG	SATFNSTEGV
21751	LQHLLRPLFQ	KSSMGPFYLG	CQLISLRPEK	DGAATGVDDT	CTYHPDPVGP
21801	GLDIQQLYWE	LSQLTHGVTQ	LGFYVLDKDS	LFINGYAPQN	LSIRGEYQIN
21851	FHIVNWNLSN	PDPTSSEYIT	LLRDIQDKVT	TLYKGSQDHD	TFRFCLVTNL
21901	TMDSVLVTVK	ALFSSNLDPS	LVEQVFLDKT	LNASFHWLGS	TYQLVDIHVT
21951	EMESSVYQPT	SSSSTQHFYL	NFTITNLPYS	QDKAQPGTTN	YQRNKRNIED
22001	ALNQLFRNSS	IKSYFSDCQV	STFRSVPNRH	HTGVDSLGNF	SPLARRVDRV
22051	AIYEFLRMT	RNGTQLQNFT	LDRSSVLVDG	YSPNRNEPLT	GNSDLPFWAV
22101	ILIGLAGLLG	LITCLICGVL	VTTRRRKKEG	EYNVQQQCPG	YYQSHLDLED
22151	LQ				



**WE CLAIM**

1. An isolated nucleic acid molecule encoding CA125.
2. The isolated nucleic acid molecule of claim 1 comprising the sequence of SEQ ID NO: 4.
3. The isolated nucleic acid molecule of claim 2 wherein the sequence has at least about 70% homology with SEQ ID NO: 4.
4. The isolated nucleic acid molecule of claim 2 wherein said molecule is a fragment thereof.
5. An isolated nucleic acid molecule comprising the sequence shown in SEQ ID NO: 1.
6. The isolated nucleic acid molecule of claim 5 wherein the sequence has at least about 70% homology with SEQ ID NO: 1.
7. The isolated nucleic acid molecule of claim 5 wherein said molecule is a fragment thereof.
8. An isolated nucleic acid molecule comprising the sequence shown in SEQ ID NO: 2.
9. The isolated nucleic acid molecule of claim 8 wherein the sequence has at least about 70% homology with SEQ ID NO: 2.
10. The isolated nucleic acid molecule of claim 8 wherein said molecule is a fragment thereof.
11. An isolated nucleic acid molecule comprising the sequence shown in SEQ ID NO: 3.
12. The isolated nucleic acid molecule of claim 11 wherein the sequence has at least about 70% homology with SEQ ID NO: 3.
13. The isolated nucleic acid molecule of claim 11 wherein said molecule is a fragment thereof.
14. A polypeptide with the amino acid sequence selected from the group consisting of: (a) the amino acid sequence set forth in SEQ ID NO: 5; (b) an amino acid sequence having at least 50% sequence identity to said sequence; (c) a conservative variant of an one of (a) to (b); and (d) a fragment of any one of (a) to (c).
15. A purified antibody that selectively binds to an amino acid sequence of the CA125 protein:
  - (a) wherein the amino acid sequence of the CA125 protein comprises the amino acid sequence set forth in SEQ ID NO: 5;

- (b) an amino acid sequence having at least 50% sequence identity to said sequence;
  - (c) a conservative variant of any one of (a) to (b); and
  - (d) a fragment of any one of (a) to (c).
16. The purified antibody of claim 15 wherein said sequence identity is at least 60%.
17. The purified antibody of claim 15 wherein said sequence identity is at least 70%.
18. The purified antibody of claim 15 wherein said sequence identity is at least 80%.
19. The purified antibody of claim 15 wherein said sequence identity is at least 90%.
20. A method to make a purified fragment of the CA125 polypeptide of SEQ ID NO: 5 comprising:
- (a) expressing a portion of the isolated nucleic acid molecule set out in SEQ ID NO: 4 to obtain a fragment of the CA125 molecule; and
  - (b) purifying said fragment of the CA125 molecule.

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SEQUENCE LISTING

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O'Brien, Timothy  
Beard, John  
Underwood, Lowell

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022438.43867(pct2).ST25.txt

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022438.43867(pct2).ST25.txt

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 2885 2890 2895  
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 3065 3070 3075  
 Leu Ser Pro Thr Ser Thr Leu Asn Met Ser Gln Glu Glu Pro Pro  
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 2630 2635 2640  
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 2675 2680 2685  
 Ser Glu Thr Ser Asn Gly Asp Ala Leu Val Leu Lys Thr Val Ser  
 2690 2695 2700  
 Asn Pro Asp Arg Ser Ile Pro Gly Ile Thr Ile Gln Gly Val Thr  
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 Glu Ser Pro Leu His Pro Ser Ser Thr Ser Pro Ser Lys Ile Val  
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 Ser Ser Glu Asn Ser Glu Thr Thr Ala Leu Val Asp Ser Ser Ala  
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 Gly Leu Glu Arg Ala Ser Val Met Pro Leu Thr Thr Gly Ser Gln  
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 Gly Met Ala Ser Ser Gly Gly Ile Arg Ser Gly Ser Thr His Ser  
 2795 2800 2805  
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 Ala Thr Gln Ser Thr Ala Pro Lys Gly Ile Pro Val Lys Pro Thr  
 2840 2845 2850

022438.43867(pct2).ST25.txt

Ile Asn Thr Ser Ile Ala Ser Ser Thr Met Asp Val Thr Lys Thr  
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 2390 2395 2400

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 2420 2425 2430

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 2435 2440 2445

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 2450 2455 2460

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Val Ser Thr Asp Thr Ala Ser Gly Glu Asn Pro Thr Ser Ser Asn  
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Ser Val Val Thr Ser Val Pro Ala Pro Gly Thr Trp Ala Ser Val  
 2495 2500 2505

Gly Ser Thr Thr Asp Leu Pro Ala Met Gly Phe Leu Lys Thr Ser  
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Pro Ala Gly Glu Ala His Ser Leu Leu Ala Ser Thr Ile Glu Pro  
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Lys Ala Ile His Ser Ser Pro Gln Thr Pro Thr Thr Pro Thr Ser  
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Gly Ala Asn Trp Glu Thr Ser Ala Thr Pro Glu Ser Leu Leu Val  
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Val Thr Glu Thr Ser Asp Thr Thr Leu Thr Ser Lys Ile Leu Val  
 2600 2605 2610

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 1940 1945 1950  
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 1955 1960 1965  
 Pro Pro Thr Ile Val Trp Thr Ser Thr Gly Thr Ile Glu Gln Ser  
 1970 1975 1980  
 Thr Gln Pro Leu His Ala Val Ser Ser Glu Lys Val Ser Val Gln  
 1985 1990 1995  
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 2000 2005 2010  
 Pro Thr His Glu Asn Ser Val Ser Ser Gly Ser Ser Thr Ser Ser  
 2015 2020 2025  
 Pro Tyr Ser Ser Ala Ser Leu Glu Ser Leu Asp Ser Thr Ile Ser  
 2030 2035 2040  
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 Leu Pro Thr Thr Thr Trp Pro Ser Thr Ser Leu Ser Glu Ala Leu  
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 Ser Ser Gly His Ser Gly Val Ser Asn Pro Ser Ser Thr Thr Thr  
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 Glu Phe Pro Leu Phe Ser Ala Ala Ser Thr Ser Ala Ala Lys Gln  
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 2105 2110 2115  
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 2120 2125 2130  
 Thr Pro Val Gly Ala Ser Ile Ser Ser Glu Val Pro Leu Pro Met  
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Arg Ser Ser Thr Ala Thr Val Ser Met Ala Gly Thr Met Gly Leu  
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 Gln Met Ser Thr Ser Ile Pro Leu Thr Ser Ser Pro Thr Thr Pro  
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 1865 1870 1875  
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 1880 1885 1890  
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022438.43867(pct2).ST25.txt

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 1655 1660 1665



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1190

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 770 775 780  
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 785 790 795 800  
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022438.43867(pct2).ST25.txt

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 Asp Ala Ser Ala Val Lys Thr Glu Thr Ser Thr Ser Glu Arg Thr  
 3650 3655 3660  
 Leu Ser Pro Ser Asp Thr Thr Ala Ser Thr Pro Ile Ser Thr Phe  
 3665 3670 3675  
 Ser Arg Val Gln Arg Met Ser Ile Ser Val Pro Asp Ile Leu Ser  
 3680 3685 3690  
 Thr Ser Trp Thr Pro Ser Ser Thr Glu Ala Glu Asp Val Pro Val  
 3695 3700 3705  
 Ser Met Val Pro Thr Asp His Ala Ser Thr Lys Thr Asp Pro Asn  
 3710 3715 3720  
 Thr Pro Leu Ser Thr Phe Leu Phe Asp Ser Leu Ser Thr Leu Asp  
 3725 3730 3735  
 Trp Asp Thr Gly Arg Ser Leu Ser Ser Ala Thr Ala Thr Thr Ser  
 3740 3745 3750  
 Ala Pro Gln Gly Ala Thr Thr Pro Gln Glu Leu Thr Leu Glu Thr  
 3755 3760 3765  
 Met Ile Ser Pro Ala Thr Ser Gln Leu Pro Phe Ser Ile Gly His  
 3770 3775 3780  
 Ile Thr Ser Ala Val Thr Pro Ala Ala Met Ala Arg Ser Ser Gly  
 3785 3790 3795

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Val Thr Phe Ser Arg Pro Asp Pro Thr Ser Lys Lys Ala Glu Gln  
 3800 3805 3810  
 Thr Ser Thr Gln Leu Pro Thr Thr Thr Ser Ala His Pro Gly Gln  
 3815 3820 3825  
 Val Pro Arg Ser Ala Ala Thr Thr Leu Asp Val Ile Pro His Thr  
 3830 3835 3840  
 Ala Lys Thr Pro Asp Ala Thr Phe Gln Arg Gln Gly Gln Thr Ala  
 3845 3850 3855  
 Leu Thr Thr Glu Ala Arg Ala Thr Ser Asp Ser Trp Asn Glu Lys  
 3860 3865 3870  
 Glu Lys Ser Thr Pro Ser Ala Pro Trp Ile Thr Glu Met Met Asn  
 3875 3880 3885  
 Ser Val Ser Glu Asp Thr Ile Lys Glu Val Thr Ser Ser Ser Ser  
 3890 3895 3900  
 Val Leu Lys Asp Pro Glu Tyr Ala Gly His Lys Leu Gly Ile Trp  
 3905 3910 3915  
 Asp Asp Phe Ile Pro Lys Phe Gly Lys Ala Ala His Met Arg Glu  
 3920 3925 3930  
 Leu Pro Leu Leu Ser Pro Pro Gln Asp Lys Glu Ala Ile His Pro  
 3935 3940 3945  
 Ser Thr Asn Thr Val Glu Thr Thr Gly Trp Val Thr Ser Ser Glu  
 3950 3955 3960  
 His Ala Ser His Ser Thr Ile Pro Ala His Ser Ala Ser Ser Lys  
 3965 3970 3975  
 Leu Thr Ser Pro Val Val Thr Thr Ser Thr Arg Glu Gln Ala Ile  
 3980 3985 3990  
 Val Ser Met Ser Thr Thr Thr Trp Pro Glu Ser Thr Arg Ala Arg  
 3995 4000 4005  
 Thr Glu Pro Asn Ser Phe Leu Thr Ile Glu Leu Arg Asp Val Ser  
 4010 4015 4020  
 Pro Tyr Met Asp Thr Ser Ser Thr Thr Gln Thr Ser Ile Ile Ser  
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4025                      4030                      4035

Ser Pro Gly Ser Thr Ala Ile Thr Lys Gly His Arg Thr Glu Ile  
4040                      4045                      4050

Thr Ser Tyr Lys Arg Ile Ser Ser Ser Phe Leu Ala Gln Ser Met  
4055                      4060                      4065

Arg Ser Ser Asp Ser Pro Ser Glu Ala Ile Thr Arg Leu Ser Asn  
4070                      4075                      4080

Phe Pro Ala Met Thr Glu Ser Gly Gly Met Ile Leu Ala Met Gln  
4085                      4090                      4095

Thr Ser Pro Pro Gly Ala Thr Ser Ile Ser Ala Pro Thr Leu Asp  
4100                      4105                      4110

Thr Ser Ala Thr Ala Ser Trp Thr Gly Thr Pro Leu Ala Thr Thr  
4115                      4120                      4125

Gln Arg Phe Thr Tyr Ser Glu Lys Thr Thr Leu Phe Ser Lys Gly  
4130                      4135                      4140

Arg Glu Asp Thr Ser Gln Pro Ser Pro Pro Cys Val Glu Glu Thr  
4145                      4150                      4155

Ser Ser Ser Ser Ser Val Val Pro Ile His Ala Thr Thr Ser Pro  
4160                      4165                      4170

Ser Asn Ile Leu Leu Thr Ser Gln Gly His Ser Pro Ser Ser Thr  
4175                      4180                      4185

Pro Pro Val Thr Ser Val Phe Leu Ser Glu Thr Ser Gly Leu Gly  
4190                      4195                      4200

Lys Thr Thr Asp Met Ser Arg Ile Ser Leu Glu Pro Gly Thr Ser  
4205                      4210                      4215

Leu Pro Pro Asn Leu Ser Ser Thr Ala Gly Glu Ala Leu Ser Thr  
4220                      4225                      4230

Tyr Glu Ala Ser Arg Asp Thr Lys Ala Ile His His Ser Ala Asp  
4235                      4240                      4245

Thr Ala Val Thr Asn Met Glu Ala Thr Ser Ser Glu Tyr Ser Pro  
4250                      4255                      4260

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Ile Pro Gly His Thr Lys Pro Ser Lys Ala Thr Ser Pro Leu Val  
 4265 4270 4275  
 Thr Ser His Ile Met Gly Asp Ile Thr Ser Ser Thr Ser Val Phe  
 4280 4285 4290  
 Gly Ser Ser Glu Thr Thr Glu Ile Glu Thr Val Ser Ser Val Asn  
 4295 4300 4305  
 Gln Gly Leu Gln Glu Arg Ser Thr Ser Gln Val Ala Ser Ser Ala  
 4310 4315 4320  
 Thr Glu Thr Ser Thr Val Ile Thr His Val Ser Ser Gly Asp Ala  
 4325 4330 4335  
 Thr Thr His Val Thr Lys Thr Gln Ala Thr Phe Ser Ser Gly Thr  
 4340 4345 4350  
 Ser Ile Ser Ser Pro His Gln Phe Ile Thr Ser Thr Asn Thr Phe  
 4355 4360 4365  
 Thr Asp Val Ser Thr Asn Pro Ser Thr Ser Leu Ile Met Thr Glu  
 4370 4375 4380  
 Ser Ser Gly Val Thr Ile Thr Thr Gln Thr Gly Pro Thr Gly Ala  
 4385 4390 4395  
 Ala Thr Gln Gly Pro Tyr Leu Leu Asp Thr Ser Thr Met Pro Tyr  
 4400 4405 4410  
 Leu Thr Glu Thr Pro Leu Ala Val Thr Pro Asp Phe Met Gln Ser  
 4415 4420 4425  
 Glu Lys Thr Thr Leu Ile Ser Lys Gly Pro Lys Asp Val Thr Trp  
 4430 4435 4440  
 Thr Ser Pro Pro Ser Val Ala Glu Thr Ser Tyr Pro Ser Ser Leu  
 4445 4450 4455  
 Thr Pro Phe Leu Val Thr Thr Ile Pro Pro Ala Thr Ser Thr Leu  
 4460 4465 4470  
 Gln Gly Gln His Thr Ser Ser Pro Val Ser Ala Thr Ser Val Leu  
 4475 4480 4485  
 Thr Ser Gly Leu Val Lys Thr Thr Asp Met Leu Asn Thr Ser Met  
 4490 4495 4500

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Glu Pro Val Thr Asn Ser Pro Gln Asn Leu Asn Asn Pro Ser Asn  
 4505 4510 4515  
 Glu Ile Leu Ala Thr Leu Ala Ala Thr Thr Asp Ile Glu Thr Ile  
 4520 4525 4530  
 His Pro Ser Ile Asn Lys Ala Val Thr Asn Met Gly Thr Ala Ser  
 4535 4540 4545  
 Ser Ala His Val Leu His Ser Thr Leu Pro Val Ser Ser Glu Pro  
 4550 4555 4560  
 Ser Thr Ala Thr Ser Pro Met Val Pro Ala Ser Ser Met Gly Asp  
 4565 4570 4575  
 Ala Leu Ala Ser Ile Ser Ile Pro Gly Ser Glu Thr Thr Asp Ile  
 4580 4585 4590  
 Glu Gly Glu Pro Thr Ser Ser Leu Thr Ala Gly Arg Lys Glu Asn  
 4595 4600 4605  
 Ser Thr Leu Gln Glu Met Asn Ser Thr Thr Glu Ser Asn Ile Ile  
 4610 4615 4620  
 Leu Ser Asn Val Ser Val Gly Ala Ile Thr Glu Ala Thr Lys Met  
 4625 4630 4635  
 Glu Val Pro Ser Phe Asp Ala Thr Phe Ile Pro Thr Pro Ala Gln  
 4640 4645 4650  
 Ser Thr Lys Phe Pro Asp Ile Phe Ser Val Ala Ser Ser Arg Leu  
 4655 4660 4665  
 Ser Asn Ser Pro Pro Met Thr Ile Ser Thr His Met Thr Thr Thr  
 4670 4675 4680  
 Gln Thr Gly Ser Ser Gly Ala Thr Ser Lys Ile Pro Leu Ala Leu  
 4685 4690 4695  
 Asp Thr Ser Thr Leu Glu Thr Ser Ala Gly Thr Pro Ser Val Val  
 4700 4705 4710  
 Thr Glu Gly Phe Ala His Ser Lys Ile Thr Thr Ala Met Asn Asn  
 4715 4720 4725  
 Asp Val Lys Asp Val Ser Gln Thr Asn Pro Pro Phe Gln Asp Glu  
 4730 4735 4740



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Ala Ser Ser Pro Ser Ser Gln Ala Pro Val Leu Val Thr Thr Leu  
 4745 4750 4755  
 Pro Ser Ser Val Ala Phe Thr Pro Gln Trp His Ser Thr Ser Ser  
 4760 4765 4770  
 Pro Val Ser Met Ser Ser Val Leu Thr Ser Ser Leu Val Lys Thr  
 4775 4780 4785  
 Ala Gly Lys Val Asp Thr Ser Leu Glu Thr Val Thr Ser Ser Pro  
 4790 4795 4800  
 Gln Ser Met Ser Asn Thr Leu Asp Asp Ile Ser Val Thr Ser Ala  
 4805 4810 4815  
 Ala Thr Thr Asp Ile Glu Thr Thr His Pro Ser Ile Asn Thr Val  
 4820 4825 4830  
 Val Thr Asn Val Gly Thr Thr Gly Ser Ala Phe Glu Ser His Ser  
 4835 4840 4845  
 Thr Val Ser Ala Tyr Pro Glu Pro Ser Lys Val Thr Ser Pro Asn  
 4850 4855 4860  
 Val Thr Thr Ser Thr Met Glu Asp Thr Thr Ile Ser Arg Ser Ile  
 4865 4870 4875  
 Pro Lys Ser Ser Lys Thr Thr Arg Thr Glu Thr Glu Thr Thr Ser  
 4880 4885 4890  
 Ser Leu Thr Pro Lys Leu Arg Glu Thr Ser Ile Ser Gln Glu Ile  
 4895 4900 4905  
 Thr Ser Ser Thr Glu Thr Ser Thr Val Pro Tyr Lys Glu Leu Thr  
 4910 4915 4920  
 Gly Ala Thr Thr Glu Val Ser Arg Thr Asp Val Thr Ser Ser Ser  
 4925 4930 4935  
 Ser Thr Ser Phe Pro Gly Pro Asp Gln Ser Thr Val Ser Leu Asp  
 4940 4945 4950  
 Ile Ser Thr Glu Thr Asn Thr Arg Leu Ser Thr Ser Pro Ile Met  
 4955 4960 4965  
 Thr Glu Ser Ala Glu Ile Thr Ile Thr Thr Gln Thr Gly Pro His  
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4970                      4975                      4980  
 Gly Ala Thr Ser Gln Asp Thr Phe Thr Met Asp Pro Ser Asn Thr  
   4985                      4990                      4995  
 Thr Pro Gln Ala Gly Ile His Ser Ala Met Thr His Gly Phe Ser  
   5000                      5005                      5010  
 Gln Leu Asp Val Thr Thr Leu Met Ser Arg Ile Pro Gln Asp Val  
   5015                      5020                      5025  
 Ser Trp Thr Ser Pro Pro Ser Val Asp Lys Thr Ser Ser Pro Ser  
   5030                      5035                      5040  
 Ser Phe Leu Ser Ser Pro Ala Met Thr Thr Pro Ser Leu Ile Ser  
   5045                      5050                      5055  
 Ser Thr Leu Pro Glu Asp Lys Leu Ser Ser Pro Met Thr Ser Leu  
   5060                      5065                      5070  
 Leu Thr Ser Gly Leu Val Lys Ile Thr Asp Ile Leu Arg Thr Arg  
   5075                      5080                      5085  
 Leu Glu Pro Val Thr Ser Ser Leu Pro Asn Phe Ser Ser Thr Ser  
   5090                      5095                      5100  
 Asp Lys Ile Leu Ala Thr Ser Lys Asp Ser Lys Asp Thr Lys Glu  
   5105                      5110                      5115  
 Ile Phe Pro Ser Ile Asn Thr Glu Glu Thr Asn Val Lys Ala Asn  
   5120                      5125                      5130  
 Asn Ser Gly His Glu Ser His Ser Pro Ala Leu Ala Asp Ser Glu  
   5135                      5140                      5145  
 Thr Pro Lys Ala Thr Thr Gln Met Val Ile Thr Thr Thr Val Gly  
   5150                      5155                      5160  
 Asp Pro Ala Pro Ser Thr Ser Met Pro Val His Gly Ser Ser Glu  
   5165                      5170                      5175  
 Thr Thr Asn Ile Lys Arg Glu Pro Thr Tyr Phe Leu Thr Pro Arg  
   5180                      5185                      5190  
 Leu Arg Glu Thr Ser Thr Ser Gln Glu Ser Ser Phe Pro Thr Asp  
   5195                      5200                      5205

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Thr Ser Phe Leu Leu Ser Lys Val Pro Thr Gly Thr Ile Thr Glu  
 5210 5215 5220  
 Val Ser Ser Thr Gly Val Ile Ser Ser Ser Lys Ile Ser Thr Pro  
 5225 5230 5235  
 Asp His Asp Lys Ser Thr Val Pro Pro Asp Thr Phe Thr Gly Glu  
 5240 5245 5250  
 Ile Pro Arg Val Phe Thr Ser Ser Ile Lys Thr Lys Ser Ala Glu  
 5255 5260 5265  
 Met Thr Ile Thr Thr Gln Ala Ser Pro Pro Glu Ser Ala Ser His  
 5270 5275 5280  
 Ser Thr Leu Pro Leu Asp Thr Ser Thr Thr Leu Ser Gln Gly Gly  
 5285 5290 5295  
 Thr His Ser Thr Val Ser Gln Gly Phe Pro Tyr Ser Glu Val Thr  
 5300 5305 5310  
 Thr Leu Met Gly Met Gly Pro Gly Asn Val Ser Trp Met Thr Thr  
 5315 5320 5325  
 Pro Pro Val Glu Glu Thr Ser Ser Val Ser Ser Leu Met Ser Ser  
 5330 5335 5340  
 Pro Ala Met Thr Ser Pro Ser Pro Val Ser Ser Thr Ser Pro Gln  
 5345 5350 5355  
 Ser Ile Pro Ser Ser Pro Leu Pro Val Thr Ala Leu Pro Thr Ser  
 5360 5365 5370  
 Val Leu Val Thr Thr Thr Asp Val Leu Gly Thr Thr Ser Pro Glu  
 5375 5380 5385  
 Ser Val Thr Ser Ser Pro Pro Asn Leu Ser Ser Ile Thr His Glu  
 5390 5395 5400  
 Arg Pro Ala Thr Tyr Lys Asp Thr Ala His Thr Glu Ala Ala Met  
 5405 5410 5415  
 His His Ser Thr Asn Thr Ala Val Thr Asn Val Gly Thr Ser Gly  
 5420 5425 5430  
 Ser Gly His Lys Ser Gln Ser Ser Val Leu Ala Asp Ser Glu Thr  
 5435 5440 5445

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Ser Lys Ala Thr Pro Leu Met Ser Thr Ala Ser Thr Leu Gly Asp  
 5450 5455 5460  
 Thr Ser Val Ser Thr Ser Thr Pro Asn Ile Ser Gln Thr Asn Gln  
 5465 5470 5475  
 Ile Gln Thr Glu Pro Thr Ala Ser Leu Ser Pro Arg Leu Arg Glu  
 5480 5485 5490  
 Ser Ser Thr Ser Glu Lys Thr Ser Ser Thr Thr Glu Thr Asn Thr  
 5495 5500 5505  
 Ala Phe Ser Tyr Val Pro Thr Gly Ala Ile Thr Gln Ala Ser Arg  
 5510 5515 5520  
 Thr Glu Ile Ser Ser Ser Arg Thr Ser Ile Ser Asp Leu Asp Arg  
 5525 5530 5535  
 Ser Thr Ile Ala Pro Asp Ile Ser Thr Gly Met Ile Thr Arg Leu  
 5540 5545 5550  
 Phe Thr Ser Pro Ile Met Thr Lys Ser Ala Glu Met Thr Val Thr  
 5555 5560 5565  
 Thr Gln Thr Thr Thr Pro Gly Ala Thr Ser Gln Gly Ile Leu Pro  
 5570 5575 5580  
 Trp Asp Thr Ser Thr Thr Leu Phe Gln Gly Gly Thr His Ser Thr  
 5585 5590 5595  
 Val Ser Gln Gly Phe Pro His Ser Glu Ile Thr Thr Leu Arg Ser  
 5600 5605 5610  
 Arg Thr Pro Gly Asp Val Ser Trp Met Thr Thr Pro Pro Val Glu  
 5615 5620 5625  
 Glu Thr Ser Ser Gly Phe Ser Leu Met Ser Pro Ser Met Thr Ser  
 5630 5635 5640  
 Pro Ser Pro Val Ser Ser Thr Ser Pro Glu Ser Ile Pro Ser Ser  
 5645 5650 5655  
 Pro Leu Pro Val Thr Ala Leu Leu Thr Ser Val Leu Val Thr Thr  
 5660 5665 5670  
 Thr Asn Val Leu Gly Thr Thr Ser Pro Glu Pro Val Thr Ser Ser  
 5675 5680 5685

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Pro Pro Asn Leu Ser Ser Pro Thr Gln Glu Arg Leu Thr Thr Tyr  
 5690 5695 5700  
 Lys Asp Thr Ala His Thr Glu Ala Met His Ala Ser Met His Thr  
 5705 5710 5715  
 Asn Thr Ala Val Ala Asn Val Gly Thr Ser Ile Ser Gly His Glu  
 5720 5725 5730  
 Ser Gln Ser Ser Val Pro Ala Asp Ser His Thr Ser Lys Ala Thr  
 5735 5740 5745  
 Ser Pro Met Gly Ile Thr Phe Ala Met Gly Asp Thr Ser Val Tyr  
 5750 5755 5760  
 Thr Ser Thr Pro Ala Phe Phe Glu Thr Arg Ile Gln Ser Glu Ser  
 5765 5770 5775  
 Thr Ser Ser Leu Ile Pro Gly Leu Arg Asp Thr Arg Thr Ser Glu  
 5780 5785 5790  
 Glu Ile Asn Thr Val Thr Glu Thr Ser Thr Val Leu Ser Glu Val  
 5795 5800 5805  
 Pro Thr Thr Thr Thr Thr Glu Val Ser Arg Thr Glu Val Ile Thr  
 5810 5815 5820  
 Ser Ser Arg Thr Thr Ile Ser Gly Pro Asp His Ser Lys Met Ser  
 5825 5830 5835  
 Pro Tyr Ile Ser Thr Glu Thr Ile Thr Arg Leu Ser Thr Phe Pro  
 5840 5845 5850  
 Phe Val Thr Gly Ser Thr Glu Met Ala Ile Thr Asn Gln Thr Gly  
 5855 5860 5865  
 Pro Ile Gly Thr Ile Ser Gln Ala Thr Leu Thr Leu Asp Thr Ser  
 5870 5875 5880  
 Ser Thr Ala Ser Trp Glu Gly Thr His Ser Pro Val Thr Gln Arg  
 5885 5890 5895  
 Phe Pro His Ser Glu Glu Thr Thr Thr Met Ser Arg Ser Thr Lys  
 5900 5905 5910  
 Gly Val Ser Trp Gln Ser Pro Pro Ser Val Glu Glu Thr Ser Ser  
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5915                      5920                      5925  
 Pro Ser Ser Pro Val Pro Leu Pro Ala Ile Thr Ser His Ser Ser  
     5930                      5935                      5940  
 Leu Tyr Ser Ala Val Ser Gly Ser Ser Pro Thr Ser Ala Leu Pro  
     5945                      5950                      5955  
 Val Thr Ser Leu Leu Thr Ser Gly Arg Arg Lys Thr Ile Asp Met  
     5960                      5965                      5970  
 Leu Asp Thr His Ser Glu Leu Val Thr Ser Ser Leu Pro Ser Ala  
     5975                      5980                      5985  
 Ser Ser Phe Ser Gly Glu Ile Leu Thr Ser Glu Ala Ser Thr Asn  
     5990                      5995                      6000  
 Thr Glu Thr Ile His Phe Ser Glu Asn Thr Ala Glu Thr Asn Met  
     6005                      6010                      6015  
 Gly Thr Thr Asn Ser Met His Lys Leu His Ser Ser Val Ser Ile  
     6020                      6025                      6030  
 His Ser Gln Pro Ser Gly His Thr Pro Pro Lys Val Thr Gly Ser  
     6035                      6040                      6045  
 Met Met Glu Asp Ala Ile Val Ser Thr Ser Thr Pro Gly Ser Pro  
     6050                      6055                      6060  
 Glu Thr Lys Asn Val Asp Arg Asp Ser Thr Ser Pro Leu Thr Pro  
     6065                      6070                      6075  
 Glu Leu Lys Glu Asp Ser Thr Ala Leu Val Met Asn Ser Thr Thr  
     6080                      6085                      6090  
 Glu Ser Asn Thr Val Phe Ser Ser Val Ser Leu Asp Ala Ala Thr  
     6095                      6100                      6105  
 Glu Val Ser Arg Ala Glu Val Thr Tyr Tyr Asp Pro Thr Phe Met  
     6110                      6115                      6120  
 Pro Ala Ser Ala Gln Ser Thr Lys Ser Pro Asp Ile Ser Pro Glu  
     6125                      6130                      6135  
 Ala Ser Ser Ser His Ser Asn Ser Pro Pro Leu Thr Ile Ser Thr  
     6140                      6145                      6150

022438.43867(pct2).ST25.txt

His Lys Thr Ile Ala Thr Gln Thr Gly Pro Ser Gly Val Thr Ser  
 6155 6160 6165  
 Leu Gly Gln Leu Thr Leu Asp Thr Ser Thr Ile Ala Thr Ser Ala  
 6170 6175 6180  
 Gly Thr Pro Ser Ala Arg Thr Gln Asp Phe Val Asp Ser Glu Thr  
 6185 6190 6195  
 Thr Ser Val Met Asn Asn Asp Leu Asn Asp Val Leu Lys Thr Ser  
 6200 6205 6210  
 Pro Phe Ser Ala Glu Glu Ala Asn Ser Leu Ser Ser Gln Ala Pro  
 6215 6220 6225  
 Leu Leu Val Thr Thr Ser Pro Ser Pro Val Thr Ser Thr Leu Gln  
 6230 6235 6240  
 Glu His Ser Thr Ser Ser Leu Val Ser Val Thr Ser Val Pro Thr  
 6245 6250 6255  
 Pro Thr Leu Ala Lys Ile Thr Asp Met Asp Thr Asn Leu Glu Pro  
 6260 6265 6270  
 Val Thr Arg Ser Pro Gln Asn Leu Arg Asn Thr Leu Ala Thr Ser  
 6275 6280 6285  
 Glu Ala Thr Thr Asp Thr His Thr Met His Pro Ser Ile Asn Thr  
 6290 6295 6300  
 Ala Met Ala Asn Val Gly Thr Thr Ser Ser Pro Asn Glu Phe Tyr  
 6305 6310 6315  
 Phe Thr Val Ser Pro Asp Ser Asp Pro Tyr Lys Ala Thr Ser Ala  
 6320 6325 6330  
 Val Val Ile Thr Ser Thr Ser Gly Asp Ser Ile Val Ser Thr Ser  
 6335 6340 6345  
 Met Pro Arg Ser Ser Ala Met Lys Lys Ile Glu Ser Glu Thr Thr  
 6350 6355 6360  
 Phe Ser Leu Ile Phe Arg Leu Arg Glu Thr Ser Thr Ser Gln Lys  
 6365 6370 6375  
 Ile Gly Ser Ser Ser Asp Thr Ser Thr Val Phe Asp Lys Ala Phe  
 6380 6385 6390

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Thr Ala Ala Thr Thr Glu Val Ser Arg Thr Glu Leu Thr Ser Ser  
6395 6400 6405

Ser Arg Thr Ser Ile Gln Gly Thr Glu Lys Pro Thr Met Ser Pro  
6410 6415 6420

Asp Thr Ser Thr Arg Ser Val Thr Met Leu Ser Thr Phe Ala Gly  
6425 6430 6435

Leu Thr Lys Ser Glu Glu Arg Thr Ile Ala Thr Gln Thr Gly Pro  
6440 6445 6450

His Arg Ala Thr Ser Gln Gly Thr Leu Thr Trp Asp Thr Ser Ile  
6455 6460 6465

Thr Thr Ser Gln Ala Gly Thr His Ser Ala Met Thr His Gly Phe  
6470 6475 6480

Ser Gln Leu Asp Leu Ser Thr Leu Thr Ser Arg Val Pro Glu Tyr  
6485 6490 6495

Ile Ser Gly Thr Ser Pro Pro Ser Val Glu Lys Thr Ser Ser Ser  
6500 6505 6510

Ser Ser Leu Leu Ser Leu Pro Ala Ile Thr Ser Pro Ser Pro Val  
6515 6520 6525

Pro Thr Thr Leu Pro Glu Ser Arg Pro Ser Ser Pro Val His Leu  
6530 6535 6540

Thr Ser Leu Pro Thr Ser Gly Leu Val Lys Thr Thr Asp Met Leu  
6545 6550 6555

Ala Ser Val Ala Ser Leu Pro Pro Asn Leu Gly Ser Thr Ser His  
6560 6565 6570

Lys Ile Pro Thr Thr Ser Gly Asp Ile Lys Asp Thr Glu Lys Met  
6575 6580 6585

Tyr Pro Ser Thr Asn Ile Ala Val Thr Asn Val Gly Thr Thr Thr  
6590 6595 6600

Ser Glu Lys Glu Ser Tyr Ser Ser Val Pro Ala Tyr Ser Glu Pro  
6605 6610 6615

Pro Lys Val Thr Ser Pro Met Val Thr Ser Phe Asn Ile Arg Asp  
6620 6625 6630



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Thr Ile Val Ser Thr Ser Met Pro Gly Ser Ser Glu Ile Thr Arg  
 6635 6640 6645  
 Ile Glu Met Glu Ser Thr Phe Ser Leu Ala His Gly Leu Lys Gly  
 6650 6655 6660  
 Thr Ser Thr Ser Gln Asp Pro Ile Val Ser Thr Glu Lys Ser Ala  
 6665 6670 6675  
 Val Leu His Lys Leu Thr Thr Gly Ala Thr Glu Thr Ser Arg Thr  
 6680 6685 6690  
 Glu Val Ala Ser Ser Arg Arg Thr Ser Ile Pro Gly Pro Asp His  
 6695 6700 6705  
 Ser Thr Glu Ser Pro Asp Ile Ser Thr Glu Val Ile Pro Ser Leu  
 6710 6715 6720  
 Pro Ile Ser Leu Gly Ile Thr Glu Ser Ser Asn Met Thr Ile Ile  
 6725 6730 6735  
 Thr Arg Thr Gly Pro Pro Leu Gly Ser Thr Ser Gln Gly Thr Phe  
 6740 6745 6750  
 Thr Leu Asp Thr Pro Thr Thr Ser Ser Arg Ala Gly Thr His Ser  
 6755 6760 6765  
 Met Ala Thr Gln Glu Phe Pro His Ser Glu Met Thr Thr Val Met  
 6770 6775 6780  
 Asn Lys Asp Pro Glu Ile Leu Ser Trp Thr Ile Pro Pro Ser Ile  
 6785 6790 6795  
 Glu Lys Thr Ser Phe Ser Ser Ser Leu Met Pro Ser Pro Ala Met  
 6800 6805 6810  
 Thr Ser Pro Pro Val Ser Ser Thr Leu Pro Lys Thr Ile His Thr  
 6815 6820 6825  
 Thr Pro Ser Pro Met Thr Ser Leu Leu Thr Pro Ser Leu Val Met  
 6830 6835 6840  
 Thr Thr Asp Thr Leu Gly Thr Ser Pro Glu Pro Thr Thr Ser Ser  
 6845 6850 6855  
 Pro Pro Asn Leu Ser Ser Thr Ser His Val Ile Leu Thr Thr Asp  
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6860                      6865                      6870  
 Glu Asp Thr Thr Ala Ile Glu Ala Met His Pro Ser Thr Ser Thr  
     6875                      6880                      6885  
 Ala Ala Thr Asn Val Glu Thr Thr Cys Ser Gly His Gly Ser Gln  
     6890                      6895                      6900  
 Ser Ser Val Leu Thr Asp Ser Glu Lys Thr Lys Ala Thr Ala Pro  
     6905                      6910                      6915  
 Met Asp Thr Thr Ser Thr Met Gly His Thr Thr Val Ser Thr Ser  
     6920                      6925                      6930  
 Met Ser Val Ser Ser Glu Thr Thr Lys Ile Lys Arg Glu Ser Thr  
     6935                      6940                      6945  
 Tyr Ser Leu Thr Pro Gly Leu Arg Glu Thr Ser Ile Ser Gln Asn  
     6950                      6955                      6960  
 Ala Ser Phe Ser Thr Asp Thr Ser Ile Val Leu Ser Glu Val Pro  
     6965                      6970                      6975  
 Thr Gly Thr Thr Ala Glu Val Ser Arg Thr Glu Val Thr Ser Ser  
     6980                      6985                      6990  
 Gly Arg Thr Ser Ile Pro Gly Pro Ser Gln Ser Thr Val Leu Pro  
     6995                      7000                      7005  
 Glu Ile Ser Thr Arg Thr Met Thr Arg Leu Phe Ala Ser Pro Thr  
     7010                      7015                      7020  
 Met Thr Glu Ser Ala Glu Met Thr Ile Pro Thr Gln Thr Gly Pro  
     7025                      7030                      7035  
 Ser Gly Ser Thr Ser Gln Asp Thr Leu Thr Leu Asp Thr Ser Thr  
     7040                      7045                      7050  
 Thr Lys Ser Gln Ala Lys Thr His Ser Thr Leu Thr Gln Arg Phe  
     7055                      7060                      7065  
 Pro His Ser Glu Met Thr Thr Leu Met Ser Arg Gly Pro Gly Asp  
     7070                      7075                      7080  
 Met Ser Trp Gln Ser Ser Pro Ser Leu Glu Asn Pro Ser Ser Leu  
     7085                      7090                      7095

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Pro Ser Leu Leu Ser Leu Pro Ala Thr Thr Ser Pro Pro Ile  
 7100 7105 7110  
 Ser Ser Thr Leu Pro Val Thr Ile Ser Ser Ser Pro Leu Pro Val  
 7115 7120 7125  
 Thr Ser Leu Leu Thr Ser Ser Pro Val Thr Thr Thr Asp Met Leu  
 7130 7135 7140  
 His Thr Ser Pro Glu Leu Val Thr Ser Ser Pro Pro Lys Leu Ser  
 7145 7150 7155  
 His Thr Ser Asp Glu Arg Leu Thr Thr Gly Lys Asp Thr Thr Asn  
 7160 7165 7170  
 Thr Glu Ala Val His Pro Ser Thr Asn Thr Ala Ala Ser Asn Val  
 7175 7180 7185  
 Glu Ile Pro Ser Phe Gly His Glu Ser Pro Ser Ser Ala Leu Ala  
 7190 7195 7200  
 Asp Ser Glu Thr Ser Lys Ala Thr Ser Pro Met Phe Ile Thr Ser  
 7205 7210 7215  
 Thr Gln Glu Asp Thr Thr Val Ala Ile Ser Thr Pro His Phe Leu  
 7220 7225 7230  
 Glu Thr Ser Arg Ile Gln Lys Glu Ser Ile Ser Ser Leu Ser Pro  
 7235 7240 7245  
 Lys Leu Arg Glu Thr Gly Ser Ser Val Glu Thr Ser Ser Ala Ile  
 7250 7255 7260  
 Glu Thr Ser Ala Val Leu Ser Glu Val Ser Ile Gly Ala Thr Thr  
 7265 7270 7275  
 Glu Ile Ser Arg Thr Glu Val Thr Ser Ser Ser Arg Thr Ser Ile  
 7280 7285 7290  
 Ser Gly Ser Ala Glu Ser Thr Met Leu Pro Glu Ile Ser Thr Thr  
 7295 7300 7305  
 Arg Lys Ile Ile Lys Phe Pro Thr Ser Pro Ile Leu Ala Glu Ser  
 7310 7315 7320  
 Ser Glu Met Thr Ile Lys Thr Gln Thr Ser Pro Pro Gly Ser Thr  
 7325 7330 7335

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Ser Glu Ser Thr Phe Thr Leu Asp Thr Ser Thr Thr Pro Ser Leu  
 7340 7345 7350  
 Val Ile Thr His Ser Thr Met Thr Gln Arg Leu Pro His Ser Glu  
 7355 7360 7365  
 Ile Thr Thr Leu Val Ser Arg Gly Ala Gly Asp Val Pro Arg Pro  
 7370 7375 7380  
 Ser Ser Leu Pro Val Glu Glu Thr Ser Pro Pro Ser Ser Gln Leu  
 7385 7390 7395  
 Ser Leu Ser Ala Met Ile Ser Pro Ser Pro Val Ser Ser Thr Leu  
 7400 7405 7410  
 Pro Ala Ser Ser His Ser Ser Ser Ala Ser Val Thr Ser Pro Leu  
 7415 7420 7425  
 Thr Pro Gly Gln Val Lys Thr Thr Glu Val Leu Asp Ala Ser Ala  
 7430 7435 7440  
 Glu Pro Glu Thr Ser Ser Pro Pro Ser Leu Ser Ser Thr Ser Val  
 7445 7450 7455  
 Glu Ile Leu Ala Thr Ser Glu Val Thr Thr Asp Thr Glu Lys Ile  
 7460 7465 7470  
 His Pro Phe Pro Asn Thr Ala Val Thr Lys Val Gly Thr Ser Ser  
 7475 7480 7485  
 Ser Gly His Glu Ser Pro Ser Ser Val Leu Pro Asp Ser Glu Thr  
 7490 7495 7500  
 Thr Lys Ala Thr Ser Ala Met Gly Thr Ile Ser Ile Met Gly Asp  
 7505 7510 7515  
 Thr Ser Val Ser Thr Leu Thr Pro Ala Leu Ser Asn Thr Arg Lys  
 7520 7525 7530  
 Ile Gln Ser Glu Pro Ala Ser Ser Leu Thr Thr Arg Leu Arg Glu  
 7535 7540 7545  
 Thr Ser Thr Ser Glu Glu Thr Ser Leu Ala Thr Glu Ala Asn Thr  
 7550 7555 7560  
 Val Leu Ser Lys Val Ser Thr Gly Ala Thr Thr Glu Val Ser Arg  
 7565 7570 7575

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Thr Glu Ala Ile Ser Phe Ser Arg Thr Ser Met Ser Gly Pro Glu  
 7580 7585 7590  
 Gln Ser Thr Met Ser Gln Asp Ile Ser Ile Gly Thr Ile Pro Arg  
 7595 7600 7605  
 Ile Ser Ala Ser Ser Val Leu Thr Glu Ser Ala Lys Met Thr Ile  
 7610 7615 7620  
 Thr Thr Gln Thr Gly Pro Ser Glu Ser Thr Leu Glu Ser Thr Leu  
 7625 7630 7635  
 Asn Leu Asn Thr Ala Thr Thr Pro Ser Trp Val Glu Thr His Ser  
 7640 7645 7650  
 Ile Val Ile Gln Gly Phe Pro His Pro Glu Met Thr Thr Ser Met  
 7655 7660 7665  
 Gly Arg Gly Pro Gly Gly Val Ser Trp Pro Ser Pro Pro Phe Val  
 7670 7675 7680  
 Lys Glu Thr Ser Pro Pro Ser Ser Pro Leu Ser Leu Pro Ala Val  
 7685 7690 7695  
 Thr Ser Pro His Pro Val Ser Thr Thr Phe Leu Ala His Ile Pro  
 7700 7705 7710  
 Pro Ser Pro Leu Pro Val Thr Ser Leu Leu Thr Ser Gly Pro Ala  
 7715 7720 7725  
 Thr Thr Thr Asp Ile Leu Gly Thr Ser Thr Glu Pro Gly Thr Ser  
 7730 7735 7740  
 Ser Ser Ser Ser Leu Ser Thr Thr Ser His Glu Arg Leu Thr Thr  
 7745 7750 7755  
 Tyr Lys Asp Thr Ala His Thr Glu Ala Val His Pro Ser Thr Asn  
 7760 7765 7770  
 Thr Gly Gly Thr Asn Val Ala Thr Thr Ser Ser Gly Tyr Lys Ser  
 7775 7780 7785  
 Gln Ser Ser Val Leu Ala Asp Ser Ser Pro Met Cys Thr Thr Ser  
 7790 7795 7800  
 Thr Met Gly Asp Thr Ser Val Leu Thr Ser Thr Pro Ala Phe Leu  
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7805                      7810                      7815  
 Glu Thr Arg Arg Ile Gln Thr Glu Leu Ala Ser Ser Leu Thr Pro  
     7820                      7825                      7830  
 Gly Leu Arg Glu Ser Ser Gly Ser Glu Gly Thr Ser Ser Gly Thr  
     7835                      7840                      7845  
 Lys Met Ser Thr Val Leu Ser Lys Val Pro Thr Gly Ala Thr Thr  
     7850                      7855                      7860  
 Glu Ile Ser Lys Glu Asp Val Thr Ser Ile Pro Gly Pro Ala Gln  
     7865                      7870                      7875  
 Ser Thr Ile Ser Pro Asp Thr Ser Thr Arg Thr Val Ser Trp Phe  
     7880                      7885                      7890  
 Ser Thr Ser Pro Val Met Thr Glu Ser Ala Glu Ile Thr Met Asn  
     7895                      7900                      7905  
 Thr His Thr Ser Pro Leu Gly Ala Thr Thr Gln Gly Thr Ser Thr  
     7910                      7915                      7920  
 Leu Asp Thr Ser Ser Thr Thr Ser Leu Thr Met Thr His Ser Thr  
     7925                      7930                      7935  
 Ile Ser Gln Gly Phe Ser His Ser Gln Met Ser Thr Leu Met Arg  
     7940                      7945                      7950  
 Arg Gly Pro Glu Asp Val Ser Trp Met Ser Pro Pro Leu Leu Glu  
     7955                      7960                      7965  
 Lys Thr Arg Pro Ser Phe Ser Leu Met Ser Ser Pro Ala Thr Thr  
     7970                      7975                      7980  
 Ser Pro Ser Pro Val Ser Ser Thr Leu Pro Glu Ser Ile Ser Ser  
     7985                      7990                      7995  
 Ser Pro Leu Pro Val Thr Ser Leu Leu Thr Ser Gly Leu Ala Lys  
     8000                      8005                      8010  
 Thr Thr Asp Met Leu His Lys Ser Ser Glu Pro Val Thr Asn Ser  
     8015                      8020                      8025  
 Pro Ala Asn Leu Ser Ser Thr Ser Val Glu Ile Leu Ala Thr Ser  
     8030                      8035                      8040

022438.43867(pct2).ST25.txt

Glu Val Thr Thr Asp Thr Glu Lys Thr His Pro Ser Ser Asn Arg  
 8045 8050 8055  
 Thr Val Thr Asp Val Gly Thr Ser Ser Ser Gly His Glu Ser Thr  
 8060 8065 8070  
 Ser Phe Val Leu Ala Asp Ser Gln Thr Ser Lys Val Thr Ser Pro  
 8075 8080 8085  
 Met Val Ile Thr Ser Thr Met Glu Asp Thr Ser Val Ser Thr Ser  
 8090 8095 8100  
 Thr Pro Gly Phe Phe Glu Thr Ser Arg Ile Gln Thr Glu Pro Thr  
 8105 8110 8115  
 Ser Ser Leu Thr Leu Gly Leu Arg Lys Thr Ser Ser Ser Glu Gly  
 8120 8125 8130  
 Thr Ser Leu Ala Thr Glu Met Ser Thr Val Leu Ser Gly Val Pro  
 8135 8140 8145  
 Thr Gly Ala Thr Ala Glu Val Ser Arg Thr Glu Val Thr Ser Ser  
 8150 8155 8160  
 Ser Arg Thr Ser Ile Ser Gly Phe Ala Gln Leu Thr Val Ser Pro  
 8165 8170 8175  
 Glu Thr Ser Thr Glu Thr Ile Thr Arg Leu Pro Thr Ser Ser Ile  
 8180 8185 8190  
 Met Thr Glu Ser Ala Glu Met Met Ile Lys Thr Gln Thr Asp Pro  
 8195 8200 8205  
 Pro Gly Ser Thr Pro Glu Ser Thr His Thr Val Asp Ile Ser Thr  
 8210 8215 8220  
 Thr Pro Asn Trp Val Glu Thr His Ser Thr Val Thr Gln Arg Phe  
 8225 8230 8235  
 Ser His Ser Glu Met Thr Thr Leu Val Ser Arg Ser Pro Gly Asp  
 8240 8245 8250  
 Met Leu Trp Pro Ser Gln Ser Ser Val Glu Glu Thr Ser Ser Ala  
 8255 8260 8265  
 Ser Ser Leu Leu Ser Leu Pro Ala Thr Thr Ser Pro Ser Pro Val  
 8270 8275 8280

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Ser Ser Thr Leu Val Glu Asp Phe Pro Ser Ala Ser Leu Pro Val  
 8285 8290 8295  
 Thr Ser Leu Leu Thr Pro Gly Leu Val Ile Thr Thr Asp Arg Met  
 8300 8305 8310  
 Gly Ile Ser Arg Glu Pro Gly Thr Ser Ser Thr Ser Asn Leu Ser  
 8315 8320 8325  
 Ser Thr Ser His Glu Arg Leu Thr Thr Leu Glu Asp Thr Val Asp  
 8330 8335 8340  
 Thr Glu Ala Met Gln Pro Ser Thr His Thr Ala Val Thr Asn Val  
 8345 8350 8355  
 Arg Thr Ser Ile Ser Gly His Glu Ser Gln Ser Ser Val Leu Ser  
 8360 8365 8370  
 Asp Ser Glu Thr Pro Lys Ala Thr Ser Ser Met Gly Thr Thr Tyr  
 8375 8380 8385  
 Thr Met Gly Glu Thr Ser Val Ser Ile Ser Thr Ser Asp Phe Phe  
 8390 8395 8400  
 Glu Thr Ser Arg Val Gln Ile Glu Pro Thr Ser Ser Leu Thr Ser  
 8405 8410 8415  
 Gly Leu Arg Glu Thr Ser Ser Ser Glu Arg Ile Ser Ser Ala Thr  
 8420 8425 8430  
 Glu Gly Ser Thr Val Leu Ser Glu Val Pro Ser Gly Ala Thr Thr  
 8435 8440 8445  
 Glu Val Ser Arg Thr Glu Val Ile Ser Ser Arg Gly Thr Ser Met  
 8450 8455 8460  
 Ser Gly Pro Asp Gln Phe Thr Ile Ser Pro Asp Ile Ser Thr Glu  
 8465 8470 8475  
 Ala Ile Thr Arg Leu Ser Thr Ser Pro Ile Met Thr Glu Ser Ala  
 8480 8485 8490  
 Glu Ser Ala Ile Thr Ile Glu Thr Gly Ser Pro Gly Ala Thr Ser  
 8495 8500 8505  
 Glu Gly Thr Leu Thr Leu Asp Thr Ser Thr Thr Thr Phe Trp Ser  
 8510 8515 8520



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Gly Thr His Ser Thr Ala Ser Pro Gly Phe Ser His Ser Glu Met  
8525 8530 8535

Thr Thr Leu Met Ser Arg Thr Pro Gly Asp Val Pro Trp Pro Ser  
8540 8545 8550

Leu Pro Ser Val Glu Glu Ala Ser Ser Val Ser Ser Ser Leu Ser  
8555 8560 8565

Ser Pro Ala Met Thr Ser Thr Ser Phe Phe Ser Ala Leu Pro Glu  
8570 8575 8580

Ser Ile Ser Ser Ser Pro His Pro Val Thr Ala Leu Leu Thr Leu  
8585 8590 8595

Gly Pro Val Lys Thr Thr Asp Met Leu Arg Thr Ser Ser Glu Pro  
8600 8605 8610

Glu Thr Ser Ser Pro Pro Asn Leu Ser Ser Thr Ser Ala Glu Ile  
8615 8620 8625

Leu Ala Thr Ser Glu Val Thr Lys Asp Arg Glu Lys Ile His Pro  
8630 8635 8640

Ser Ser Asn Thr Pro Val Val Asn Val Gly Thr Val Ile Tyr Lys  
8645 8650 8655

His Leu Ser Pro Ser Ser Val Leu Ala Asp Leu Val Thr Thr Lys  
8660 8665 8670

Pro Thr Ser Pro Met Ala Thr Thr Ser Thr Leu Gly Asn Thr Ser  
8675 8680 8685

Val Ser Thr Ser Thr Pro Ala Phe Pro Glu Thr Met Met Thr Gln  
8690 8695 8700

Pro Thr Ser Ser Leu Thr Ser Gly Leu Arg Glu Ile Ser Thr Ser  
8705 8710 8715

Gln Glu Thr Ser Ser Ala Thr Glu Arg Ser Ala Ser Leu Ser Gly  
8720 8725 8730

Met Pro Thr Gly Ala Thr Thr Lys Val Ser Arg Thr Glu Ala Leu  
8735 8740 8745

Ser Leu Gly Arg Thr Ser Thr Pro Gly Pro Ala Gln Ser Thr Ile  
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8750 022438.43867(pct2).ST25.txt  
 8755 8760  
 Ser Pro Glu Ile Ser Thr Glu Thr Ile Thr Arg Ile Ser Thr Pro  
 8765 8770 8775  
 Leu Thr Thr Thr Gly Ser Ala Glu Met Thr Ile Thr Pro Lys Thr  
 8780 8785 8790  
 Gly His Ser Gly Ala Ser Ser Gln Gly Thr Phe Thr Leu Asp Thr  
 8795 8800 8805  
 Ser Ser Arg Ala Ser Trp Pro Gly Thr His Ser Ala Ala Thr His  
 8810 8815 8820  
 Arg Ser Pro His Ser Gly Met Thr Thr Pro Met Ser Arg Gly Pro  
 8825 8830 8835  
 Glu Asp Val Ser Trp Pro Ser Arg Pro Ser Val Glu Lys Thr Ser  
 8840 8845 8850  
 Pro Pro Ser Ser Leu Val Ser Leu Ser Ala Val Thr Ser Pro Ser  
 8855 8860 8865  
 Pro Leu Tyr Ser Thr Pro Ser Glu Ser Ser His Ser Ser Pro Leu  
 8870 8875 8880  
 Arg Val Thr Ser Leu Phe Thr Pro Val Met Met Lys Thr Thr Asp  
 8885 8890 8895  
 Met Leu Asp Thr Ser Leu Glu Pro Val Thr Thr Ser Pro Pro Ser  
 8900 8905 8910  
 Met Asn Ile Thr Ser Asp Glu Ser Leu Ala Thr Ser Lys Ala Thr  
 8915 8920 8925  
 Met Glu Thr Glu Ala Ile Gln Leu Ser Glu Asn Thr Ala Val Thr  
 8930 8935 8940  
 Gln Met Gly Thr Ile Ser Ala Arg Gln Glu Phe Tyr Ser Ser Tyr  
 8945 8950 8955  
 Pro Gly Leu Pro Glu Pro Ser Lys Val Thr Ser Pro Val Val Thr  
 8960 8965 8970  
 Ser Ser Thr Ile Lys Asp Ile Val Ser Thr Thr Ile Pro Ala Ser  
 8975 8980 8985

022438.43867(pct2).ST25.txt

Ser Glu Ile Thr Arg Ile Glu Met Glu Ser Thr Ser Thr Leu Thr  
 8990 8995 9000  
 Pro Thr Pro Arg Glu Thr Ser Thr Ser Gln Glu Ile His Ser Ala  
 9005 9010 9015  
 Thr Lys Pro Ser Thr Val Pro Tyr Lys Ala Leu Thr Ser Ala Thr  
 9020 9025 9030  
 Ile Glu Asp Ser Met Thr Gln Val Met Ser Ser Ser Arg Gly Pro  
 9035 9040 9045  
 Ser Pro Asp Gln Ser Thr Met Ser Gln Asp Ile Ser Thr Glu Val  
 9050 9055 9060  
 Ile Thr Arg Leu Ser Thr Ser Pro Ile Lys Ala Glu Ser Thr Glu  
 9065 9070 9075  
 Met Thr Ile Thr Thr Gln Thr Gly Ser Pro Gly Ala Thr Ser Arg  
 9080 9085 9090  
 Gly Thr Leu Thr Leu Asp Thr Ser Thr Thr Phe Met Ser Gly Thr  
 9095 9100 9105  
 His Ser Thr Ala Ser Gln Gly Phe Ser His Ser Gln Met Thr Ala  
 9110 9115 9120  
 Leu Met Ser Arg Thr Pro Gly Asp Val Pro Trp Leu Ser His Pro  
 9125 9130 9135  
 Ser Val Glu Glu Ala Ser Ser Ala Ser Phe Ser Leu Ser Ser Pro  
 9140 9145 9150  
 Val Met Thr Ser Ser Ser Pro Val Ser Ser Thr Leu Pro Asp Ser  
 9155 9160 9165  
 Ile His Ser Ser Ser Leu Pro Val Thr Ser Leu Leu Thr Ser Gly  
 9170 9175 9180  
 Leu Val Lys Thr Thr Glu Leu Leu Gly Thr Ser Ser Glu Pro Glu  
 9185 9190 9195  
 Thr Ser Ser Pro Pro Asn Leu Ser Ser Thr Ser Ala Glu Ile Leu  
 9200 9205 9210  
 Ala Thr Thr Glu Val Thr Thr Asp Thr Glu Lys Leu Glu Met Thr  
 9215 9220 9225

022438.43867(pct2).ST25.txt

Asn Val Val Thr Ser Gly Tyr Thr His Glu Ser Pro Ser Ser Val  
 9230 9235 9240  
 Leu Ala Asp Ser Val Thr Thr Lys Ala Thr Ser Ser Met Gly Ile  
 9245 9250 9255  
 Thr Tyr Pro Thr Gly Asp Thr Asn Val Leu Thr Ser Thr Pro Ala  
 9260 9265 9270  
 Phe Ser Asp Thr Ser Arg Ile Gln Thr Lys Ser Lys Leu Ser Leu  
 9275 9280 9285  
 Thr Pro Gly Leu Met Glu Thr Ser Ile Ser Glu Glu Thr Ser Ser  
 9290 9295 9300  
 Ala Thr Glu Lys Ser Thr Val Leu Ser Ser Val Pro Thr Gly Ala  
 9305 9310 9315  
 Thr Thr Glu Val Ser Arg Thr Glu Ala Ile Ser Ser Ser Arg Thr  
 9320 9325 9330  
 Ser Ile Pro Gly Pro Ala Gln Ser Thr Met Ser Ser Asp Thr Ser  
 9335 9340 9345  
 Met Glu Thr Ile Thr Arg Ile Ser Thr Pro Leu Thr Arg Lys Glu  
 9350 9355 9360  
 Ser Thr Asp Met Ala Ile Thr Pro Lys Thr Gly Pro Ser Gly Ala  
 9365 9370 9375  
 Thr Ser Gln Gly Thr Phe Thr Leu Asp Ser Ser Ser Thr Ala Ser  
 9380 9385 9390  
 Trp Pro Gly Thr His Ser Ala Thr Thr Gln Arg Phe Pro Gln Ser  
 9395 9400 9405  
 Val Val Thr Thr Pro Met Ser Arg Gly Pro Glu Asp Val Ser Trp  
 9410 9415 9420  
 Pro Ser Pro Leu Ser Val Glu Lys Asn Ser Pro Pro Ser Ser Leu  
 9425 9430 9435  
 Val Ser Ser Ser Ser Val Thr Ser Pro Ser Pro Leu Tyr Ser Thr  
 9440 9445 9450  
 Pro Ser Gly Ser Ser His Ser Ser Pro Val Pro Val Thr Ser Leu  
 9455 9460 9465

022438.43867(pct2).ST25.txt

Phe Thr Ser Ile Met Met Lys Ala Thr Asp Met Leu Asp Ala Ser  
 9470 9475 9480  
 Leu Glu Pro Glu Thr Thr Ser Ala Pro Asn Met Asn Ile Thr Ser  
 9485 9490 9495  
 Asp Glu Ser Leu Ala Thr Ser Lys Ala Thr Thr Glu Thr Glu Ala  
 9500 9505 9510  
 Ile His Val Phe Glu Asn Thr Ala Ala Ser His Val Glu Thr Thr  
 9515 9520 9525  
 Ser Ala Thr Glu Glu Leu Tyr Ser Ser Ser Pro Gly Phe Ser Glu  
 9530 9535 9540  
 Pro Thr Lys Val Ile Ser Pro Val Val Thr Ser Ser Ser Ile Arg  
 9545 9550 9555  
 Asp Asn Met Val Ser Thr Thr Met Pro Gly Ser Ser Gly Ile Thr  
 9560 9565 9570  
 Arg Ile Glu Ile Glu Ser Met Ser Ser Leu Thr Pro Gly Leu Arg  
 9575 9580 9585  
 Glu Thr Arg Thr Ser Gln Asp Ile Thr Ser Ser Thr Glu Thr Ser  
 9590 9595 9600  
 Thr Val Leu Tyr Lys Met Ser Ser Gly Ala Thr Pro Glu Val Ser  
 9605 9610 9615  
 Arg Thr Glu Val Met Pro Ser Ser Arg Thr Ser Ile Pro Gly Pro  
 9620 9625 9630  
 Ala Gln Ser Thr Met Ser Leu Asp Ile Ser Asp Glu Val Val Thr  
 9635 9640 9645  
 Arg Leu Ser Thr Ser Pro Ile Met Thr Glu Ser Ala Glu Ile Thr  
 9650 9655 9660  
 Ile Thr Thr Gln Thr Gly Tyr Ser Leu Ala Thr Ser Gln Val Thr  
 9665 9670 9675  
 Leu Pro Leu Gly Thr Ser Met Thr Phe Leu Ser Gly Thr His Ser  
 9680 9685 9690  
 Thr Met Ser Gln Gly Leu Ser His Ser Glu Met Thr Asn Leu Met  
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9695 022438.43867(pct2).ST25.txt  
 9700 9705  
 Ser Arg Gly Pro Glu Ser Leu Ser Trp Thr Ser Pro Arg Phe Val  
 9710 9715 9720  
 Glu Thr Thr Arg Ser Ser Ser Ser Leu Thr Ser Leu Pro Leu Thr  
 9725 9730 9735  
 Thr Ser Leu Ser Pro Val Ser Ser Thr Leu Leu Asp Ser Ser Pro  
 9740 9745 9750  
 Ser Ser Pro Leu Pro Val Thr Ser Leu Ile Leu Pro Gly Leu Val  
 9755 9760 9765  
 Lys Thr Thr Glu Val Leu Asp Thr Ser Ser Glu Pro Lys Thr Ser  
 9770 9775 9780  
 Ser Ser Pro Asn Leu Ser Ser Thr Ser Val Glu Ile Pro Ala Thr  
 9785 9790 9795  
 Ser Glu Ile Met Thr Asp Thr Glu Lys Ile His Pro Ser Ser Asn  
 9800 9805 9810  
 Thr Ala Val Ala Lys Val Arg Thr Ser Ser Ser Val His Glu Ser  
 9815 9820 9825  
 His Ser Ser Val Leu Ala Asp Ser Glu Thr Thr Ile Thr Ile Pro  
 9830 9835 9840  
 Ser Met Gly Ile Thr Ser Ala Val Asp Asp Thr Thr Val Phe Thr  
 9845 9850 9855  
 Ser Asn Pro Ala Phe Ser Glu Thr Arg Arg Ile Pro Thr Glu Pro  
 9860 9865 9870  
 Thr Phe Ser Leu Thr Pro Gly Phe Arg Glu Thr Ser Thr Ser Glu  
 9875 9880 9885  
 Glu Thr Thr Ser Ile Thr Glu Thr Ser Ala Val Leu Tyr Gly Val  
 9890 9895 9900  
 Pro Thr Ser Ala Thr Thr Glu Val Ser Met Thr Glu Ile Met Ser  
 9905 9910 9915  
 Ser Asn Arg Thr His Ile Pro Asp Ser Asp Gln Ser Thr Met Ser  
 9920 9925 9930

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Pro Asp Ile Ile Thr Glu Val Ile Thr Arg Leu Ser Ser Ser  
9935 9940 9945

Met Met Ser Glu Ser Thr Gln Met Thr Ile Thr Thr Gln Lys Ser  
9950 9955 9960

Ser Pro Gly Ala Thr Ala Gln Ser Thr Leu Thr Leu Ala Thr Thr  
9965 9970 9975

Thr Ala Pro Leu Ala Arg Thr His Ser Thr Val Pro Pro Arg Phe  
9980 9985 9990

Leu His Ser Glu Met Thr Thr Leu Met Ser Arg Ser Pro Glu Asn  
9995 10000 10005

Pro Ser Trp Lys Ser Ser Pro Phe Val Glu Lys Thr Ser Ser Ser  
10010 10015 10020

Ser Ser Leu Leu Ser Leu Pro Val Thr Thr Ser Pro Ser Val Ser  
10025 10030 10035

Ser Thr Leu Pro Gln Ser Ile Pro Ser Ser Ser Phe Ser Val Thr  
10040 10045 10050

Ser Leu Leu Thr Pro Gly Met Val Lys Thr Thr Asp Thr Ser Thr  
10055 10060 10065

Glu Pro Gly Thr Ser Leu Ser Pro Asn Leu Ser Gly Thr Ser Val  
10070 10075 10080

Glu Ile Leu Ala Ala Ser Glu Val Thr Thr Asp Thr Glu Lys Ile  
10085 10090 10095

His Pro Ser Ser Ser Met Ala Val Thr Asn Val Gly Thr Thr Ser  
10100 10105 10110

Ser Gly His Glu Leu Tyr Ser Ser Val Ser Ile His Ser Glu Pro  
10115 10120 10125

Ser Lys Ala Thr Tyr Pro Val Gly Thr Pro Ser Ser Met Ala Glu  
10130 10135 10140

Thr Ser Ile Ser Thr Ser Met Pro Ala Asn Phe Glu Thr Thr Gly  
10145 10150 10155

Phe Glu Ala Glu Pro Phe Ser His Leu Thr Ser Gly Phe Arg Lys  
10160 10165 10170

022438.43867(pct2).ST25.txt

Thr Asn Met Ser Leu Asp Thr Ser Ser Val Thr Pro Thr Asn Thr  
 10175 10180 10185  
 Pro Ser Ser Pro Gly Ser Thr His Leu Leu Gln Ser Ser Lys Thr  
 10190 10195 10200  
 Asp Phe Thr Ser Ser Ala Lys Thr Ser Ser Pro Asp Trp Pro Pro  
 10205 10210 10215  
 Ala Ser Gln Tyr Thr Glu Ile Pro Val Asp Ile Ile Thr Pro Phe  
 10220 10225 10230  
 Asn Ala Ser Pro Ser Ile Thr Glu Ser Thr Gly Ile Thr Ser Phe  
 10235 10240 10245  
 Pro Glu Ser Arg Phe Thr Met Ser Val Thr Glu Ser Thr His His  
 10250 10255 10260  
 Leu Ser Thr Asp Leu Leu Pro Ser Ala Glu Thr Ile Ser Thr Gly  
 10265 10270 10275  
 Thr Val Met Pro Ser Leu Ser Glu Ala Met Thr Ser Phe Ala Thr  
 10280 10285 10290  
 Thr Gly Val Pro Arg Ala Ile Ser Gly Ser Gly Ser Pro Phe Ser  
 10295 10300 10305  
 Arg Thr Glu Ser Gly Pro Gly Asp Ala Thr Leu Ser Thr Ile Ala  
 10310 10315 10320  
 Glu Ser Leu Pro Ser Ser Thr Pro Val Pro Phe Ser Ser Ser Thr  
 10325 10330 10335  
 Phe Thr Thr Thr Asp Ser Ser Thr Ile Pro Ala Leu His Glu Ile  
 10340 10345 10350  
 Thr Ser Ser Ser Ala Thr Pro Tyr Arg Val Asp Thr Ser Leu Gly  
 10355 10360 10365  
 Thr Glu Ser Ser Thr Thr Glu Gly Arg Leu Val Met Val Ser Thr  
 10370 10375 10380  
 Leu Asp Thr Ser Ser Gln Pro Gly Arg Thr Ser Ser Thr Pro Ile  
 10385 10390 10395  
 Leu Asp Thr Arg Met Thr Glu Ser Val Glu Leu Gly Thr Val Thr  
 10400 10405 10410



022438.43867(pct2).ST25.txt

Ser Ala Tyr Gln Val Pro Ser Leu Ser Thr Arg Leu Thr Arg Thr  
 10415 10420 10425  
 Asp Gly Ile Met Glu His Ile Thr Lys Ile Pro Asn Glu Ala Ala  
 10430 10435 10440  
 His Arg Gly Thr Ile Arg Pro Val Lys Gly Pro Gln Thr Ser Thr  
 10445 10450 10455  
 Ser Pro Ala Ser Pro Lys Gly Leu His Thr Gly Gly Thr Lys Arg  
 10460 10465 10470  
 Met Glu Thr Thr Thr Thr Ala Leu Lys Thr Thr Thr Thr Ala Leu  
 10475 10480 10485  
 Lys Thr Thr Ser Arg Ala Thr Leu Thr Thr Ser Val Tyr Thr Pro  
 10490 10495 10500  
 Thr Leu Gly Thr Leu Thr Pro Leu Asn Ala Ser Arg Gln Met Ala  
 10505 10510 10515  
 Ser Thr Ile Leu Thr Glu Met Met Ile Thr Thr Pro Tyr Val Phe  
 10520 10525 10530  
 Pro Asp Val Pro Glu Thr Thr Ser Ser Leu Ala Thr Ser Leu Gly  
 10535 10540 10545  
 Ala Glu Thr Ser Thr Ala Leu Pro Arg Thr Thr Pro Ser Val Leu  
 10550 10555 10560  
 Asn Arg Glu Ser Glu Thr Thr Ala Ser Leu Val Ser Arg Ser Gly  
 10565 10570 10575  
 Ala Glu Arg Ser Pro Val Ile Gln Thr Leu Asp Val Ser Ser Ser  
 10580 10585 10590  
 Glu Pro Asp Thr Thr Ala Ser Trp Val Ile His Pro Ala Glu Thr  
 10595 10600 10605  
 Ile Pro Thr Val Ser Lys Thr Thr Pro Asn Phe Phe His Ser Glu  
 10610 10615 10620  
 Leu Asp Thr Val Ser Ser Thr Ala Thr Ser His Gly Ala Asp Val  
 10625 10630 10635  
 Ser Ser Ala Ile Pro Thr Asn Ile Ser Pro Ser Glu Leu Asp Ala  
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10640

10645

10650

Leu	Thr	Pro	Leu	Val	Thr	Ile	Ser	Gly	Thr	Asp	Thr	Ser	Thr	Thr
	10655					10660					10665			
Phe	Pro	Thr	Leu	Thr	Lys	Ser	Pro	His	Glu	Thr	Glu	Thr	Arg	Thr
	10670					10675					10680			
Thr	Trp	Leu	Thr	His	Pro	Ala	Glu	Thr	Ser	Ser	Thr	Ile	Pro	Arg
	10685					10690					10695			
Thr	Ile	Pro	Asn	Phe	Ser	His	His	Glu	Ser	Asp	Ala	Thr	Pro	Ser
	10700					10705					10710			
Ile	Ala	Thr	Ser	Pro	Gly	Ala	Glu	Thr	Ser	Ser	Ala	Ile	Pro	Ile
	10715					10720					10725			
Met	Thr	Val	Ser	Pro	Gly	Ala	Glu	Asp	Leu	Val	Thr	Ser	Gln	Val
	10730					10735					10740			
Thr	Ser	Ser	Gly	Thr	Asp	Arg	Asn	Met	Thr	Ile	Pro	Thr	Leu	Thr
	10745					10750					10755			
Leu	Ser	Pro	Gly	Glu	Pro	Lys	Thr	Ile	Ala	Ser	Leu	Val	Thr	His
	10760					10765					10770			
Pro	Glu	Ala	Gln	Thr	Ser	Ser	Ala	Ile	Pro	Thr	Ser	Thr	Ile	Ser
	10775					10780					10785			
Pro	Ala	Val	Ser	Arg	Leu	Val	Thr	Ser	Met	Val	Thr	Ser	Leu	Ala
	10790					10795					10800			
Ala	Lys	Thr	Ser	Thr	Thr	Asn	Arg	Ala	Leu	Thr	Asn	Ser	Pro	Gly
	10805					10810					10815			
Glu	Pro	Ala	Thr	Thr	Val	Ser	Leu	Val	Thr	His	Pro	Ala	Gln	Thr
	10820					10825					10830			
Ser	Pro	Thr	Val	Pro	Trp	Thr	Thr	Ser	Ile	Phe	Phe	His	Ser	Lys
	10835					10840					10845			
Ser	Asp	Thr	Thr	Pro	Ser	Met	Thr	Thr	Ser	His	Gly	Ala	Glu	Ser
	10850					10855					10860			
Ser	Ser	Ala	Val	Pro	Thr	Pro	Thr	Val	Ser	Thr	Glu	Val	Pro	Gly
	10865					10870					10875			

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Val	Val	Thr	Pro	Leu	Val	Thr	Ser	Ser	Arg	Ala	Val	Ile	Ser	Thr
	10880					10885					10890			
Thr	Ile	Pro	Ile	Leu	Thr	Leu	Ser	Pro	Gly	Glu	Pro	Glu	Thr	Thr
	10895					10900					10905			
Pro	Ser	Met	Ala	Thr	Ser	His	Gly	Glu	Glu	Ala	Ser	Ser	Ala	Ile
	10910					10915					10920			
Pro	Thr	Pro	Thr	Val	Ser	Pro	Gly	Val	Pro	Gly	Val	Val	Thr	Ser
	10925					10930					10935			
Leu	Val	Thr	Ser	Ser	Arg	Ala	Val	Thr	Ser	Thr	Thr	Ile	Pro	Ile
	10940					10945					10950			
Leu	Thr	Phe	Ser	Leu	Gly	Glu	Pro	Glu	Thr	Thr	Pro	Ser	Met	Ala
	10955					10960					10965			
Thr	Ser	His	Gly	Thr	Glu	Ala	Gly	Ser	Ala	Val	Pro	Thr	Val	Leu
	10970					10975					10980			
Pro	Glu	Val	Pro	Gly	Met	Val	Thr	Ser	Leu	Val	Ala	Ser	Ser	Arg
	10985					10990					10995			
Ala	Val	Thr	Ser	Thr	Thr	Leu	Pro	Thr	Leu	Thr	Leu	Ser	Pro	Gly
	11000					11005					11010			
Glu	Pro	Glu	Thr	Thr	Pro	Ser	Met	Ala	Thr	Ser	His	Gly	Ala	Glu
	11015					11020					11025			
Ala	Ser	Ser	Thr	Val	Pro	Thr	Val	Ser	Pro	Glu	Val	Pro	Gly	Val
	11030					11035					11040			
Val	Thr	Ser	Leu	Val	Thr	Ser	Ser	Ser	Gly	Val	Asn	Ser	Thr	Ser
	11045					11050					11055			
Ile	Pro	Thr	Leu	Ile	Leu	Ser	Pro	Gly	Glu	Leu	Glu	Thr	Thr	Pro
	11060					11065					11070			
Ser	Met	Ala	Thr	Ser	His	Gly	Ala	Glu	Ala	Ser	Ser	Ala	Val	Pro
	11075					11080					11085			
Thr	Pro	Thr	Val	Ser	Pro	Gly	Val	Ser	Gly	Val	Val	Thr	Pro	Leu
	11090					11095					11100			
Val	Thr	Ser	Ser	Arg	Ala	Val	Thr	Ser	Thr	Thr	Ile	Pro	Ile	Leu
	11105					11110					11115			

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Thr Leu Ser Ser Ser Glu Pro Glu Thr Thr Pro Ser Met Ala Thr  
 11120 11125 11130  
 Ser His Gly Val Glu Ala Ser Ser Ala Val Leu Thr Val Ser Pro  
 11135 11140 11145  
 Glu Val Pro Gly Met Val Thr Ser Leu Val Thr Ser Ser Arg Ala  
 11150 11155 11160  
 Val Thr Ser Thr Thr Ile Pro Thr Leu Thr Ile Ser Ser Asp Glu  
 11165 11170 11175  
 Pro Glu Thr Thr Thr Ser Leu Val Thr His Ser Glu Ala Lys Met  
 11180 11185 11190  
 Ile Ser Ala Ile Pro Thr Leu Ala Val Ser Pro Thr Val Gln Gly  
 11195 11200 11205  
 Leu Val Thr Ser Leu Val Thr Ser Ser Gly Ser Glu Thr Ser Ala  
 11210 11215 11220  
 Phe Ser Asn Leu Thr Val Ala Ser Ser Gln Pro Glu Thr Ile Asp  
 11225 11230 11235  
 Ser Trp Val Ala His Pro Gly Thr Glu Ala Ser Ser Val Val Pro  
 11240 11245 11250  
 Thr Leu Thr Val Ser Thr Gly Glu Pro Phe Thr Asn Ile Ser Leu  
 11255 11260 11265  
 Val Thr His Pro Ala Glu Ser Ser Ser Thr Leu Pro Arg Thr Thr  
 11270 11275 11280  
 Ser Arg Phe Ser His Ser Glu Leu Asp Thr Met Pro Ser Thr Val  
 11285 11290 11295  
 Thr Ser Pro Glu Ala Glu Ser Ser Ser Ala Ile Ser Thr Thr Ile  
 11300 11305 11310  
 Ser Pro Gly Ile Pro Gly Val Leu Thr Ser Leu Val Thr Ser Ser  
 11315 11320 11325  
 Gly Arg Asp Ile Ser Ala Thr Phe Pro Thr Val Pro Glu Ser Pro  
 11330 11335 11340  
 His Glu Ser Glu Ala Thr Ala Ser Trp Val Thr His Pro Ala Val  
 11345 11350 11355

022438.43867(pct2).ST25.txt

Thr Ser Thr Thr Val Pro Arg Thr Thr Pro Asn Tyr Ser His Ser  
 11360 11365 11370  
 Glu Pro Asp Thr Thr Pro Ser Ile Ala Thr Ser Pro Gly Ala Glu  
 11375 11380 11385  
 Ala Thr Ser Asp Phe Pro Thr Ile Thr Val Ser Pro Asp Val Pro  
 11390 11395 11400  
 Asp Met Val Thr Ser Gln Val Thr Ser Ser Gly Thr Asp Thr Ser  
 11405 11410 11415  
 Ile Thr Ile Pro Thr Leu Thr Leu Ser Ser Gly Glu Pro Glu Thr  
 11420 11425 11430  
 Thr Thr Ser Phe Ile Thr Tyr Ser Glu Thr His Thr Ser Ser Ala  
 11435 11440 11445  
 Ile Pro Thr Leu Pro Val Ser Pro Gly Ala Ser Lys Met Leu Thr  
 11450 11455 11460  
 Ser Leu Val Ile Ser Ser Gly Thr Asp Ser Thr Thr Thr Phe Pro  
 11465 11470 11475  
 Thr Leu Thr Glu Thr Pro Tyr Glu Pro Glu Thr Thr Ala Ile Gln  
 11480 11485 11490  
 Leu Ile His Pro Ala Glu Thr Asn Thr Met Val Pro Arg Thr Thr  
 11495 11500 11505  
 Pro Lys Phe Ser His Ser Lys Ser Asp Thr Thr Leu Pro Val Ala  
 11510 11515 11520  
 Ile Thr Ser Pro Gly Pro Glu Ala Ser Ser Ala Val Ser Thr Thr  
 11525 11530 11535  
 Thr Ile Ser Pro Asp Met Ser Asp Leu Val Thr Ser Leu Val Pro  
 11540 11545 11550  
 Ser Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr Leu Ser Glu  
 11555 11560 11565  
 Thr Pro Tyr Glu Pro Glu Thr Thr Ala Thr Trp Leu Thr His Pro  
 11570 11575 11580  
 Ala Glu Thr Ser Thr Thr Val Ser Gly Thr Ile Pro Asn Phe Ser  
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11585 022438.43867(pct2).ST25.txt  
 11590 11595  
 His Arg Gly Ser Asp Thr Ala Pro Ser Met Val Thr Ser Pro Gly  
 11600 11605 11610  
 Val Asp Thr Arg Ser Gly Val Pro Thr Thr Thr Ile Pro Pro Ser  
 11615 11620 11625  
 Ile Pro Gly Val Val Thr Ser Gln Val Thr Ser Ser Ala Thr Asp  
 11630 11635 11640  
 Thr Ser Thr Ala Ile Pro Thr Leu Thr Pro Ser Pro Gly Glu Pro  
 11645 11650 11655  
 Glu Thr Thr Ala Ser Ser Ala Thr His Pro Gly Thr Gln Thr Gly  
 11660 11665 11670  
 Phe Thr Val Pro Ile Arg Thr Val Pro Ser Ser Glu Pro Asp Thr  
 11675 11680 11685  
 Met Ala Ser Trp Val Thr His Pro Pro Gln Thr Ser Thr Pro Val  
 11690 11695 11700  
 Ser Arg Thr Thr Ser Ser Phe Ser His Ser Ser Pro Asp Ala Thr  
 11705 11710 11715  
 Pro Val Met Ala Thr Ser Pro Arg Thr Glu Ala Ser Ser Ala Val  
 11720 11725 11730  
 Leu Thr Thr Ile Ser Pro Gly Ala Pro Glu Met Val Thr Ser Gln  
 11735 11740 11745  
 Ile Thr Ser Ser Gly Ala Ala Thr Ser Thr Thr Val Pro Thr Leu  
 11750 11755 11760  
 Thr His Ser Pro Gly Met Pro Glu Thr Thr Ala Leu Leu Ser Thr  
 11765 11770 11775  
 His Pro Arg Thr Glu Thr Ser Lys Thr Phe Pro Ala Ser Thr Val  
 11780 11785 11790  
 Phe Pro Gln Val Ser Glu Thr Thr Ala Ser Leu Thr Ile Arg Pro  
 11795 11800 11805  
 Gly Ala Glu Thr Ser Thr Ala Leu Pro Thr Gln Thr Thr Ser Ser  
 11810 11815 11820

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Leu	Phe	Thr	Leu	Leu	Val	Thr	Gly	Thr	Ser	Arg	Val	Asp	Leu	Ser
11825						11830					11835			
Pro	Thr	Ala	Ser	Pro	Gly	Val	Ser	Ala	Lys	Thr	Ala	Pro	Leu	Ser
11840						11845					11850			
Thr	His	Pro	Gly	Thr	Glu	Thr	Ser	Thr	Met	Ile	Pro	Thr	Ser	Thr
11855						11860					11865			
Leu	Ser	Leu	Gly	Leu	Leu	Glu	Thr	Thr	Gly	Leu	Leu	Ala	Thr	Ser
11870						11875					11880			
Ser	Ser	Ala	Glu	Thr	Ser	Thr	Ser	Thr	Leu	Thr	Leu	Thr	Val	Ser
11885						11890					11895			
Pro	Ala	Val	Ser	Gly	Leu	Ser	Ser	Ala	Ser	Ile	Thr	Thr	Asp	Lys
11900						11905					11910			
Pro	Gln	Thr	Val	Thr	Ser	Trp	Asn	Thr	Glu	Thr	Ser	Pro	Ser	Val
11915						11920					11925			
Thr	Ser	Val	Gly	Pro	Pro	Glu	Phe	Ser	Arg	Thr	Val	Thr	Gly	Thr
11930						11935					11940			
Thr	Met	Thr	Leu	Ile	Pro	Ser	Glu	Met	Pro	Thr	Pro	Pro	Lys	Thr
11945						11950					11955			
Ser	His	Gly	Glu	Gly	Val	Ser	Pro	Thr	Thr	Ile	Leu	Arg	Thr	Thr
11960						11965					11970			
Met	Val	Glu	Ala	Thr	Asn	Leu	Ala	Thr	Thr	Gly	Ser	Ser	Pro	Thr
11975						11980					11985			
Val	Ala	Lys	Thr	Thr	Thr	Thr	Phe	Asn	Thr	Leu	Ala	Gly	Ser	Leu
11990						11995					12000			
Phe	Thr	Pro	Leu	Thr	Thr	Pro	Gly	Met	Ser	Thr	Leu	Ala	Ser	Glu
12005						12010					12015			
Ser	Val	Thr	Ser	Arg	Thr	Ser	Tyr	Asn	His	Arg	Ser	Trp	Ile	Ser
12020						12025					12030			
Thr	Thr	Ser	Ser	Tyr	Asn	Arg	Arg	Tyr	Trp	Thr	Pro	Ala	Thr	Ser
12035						12040					12045			
Thr	Pro	Val	Thr	Ser	Thr	Phe	Ser	Pro	Gly	Ile	Ser	Thr	Ser	Ser
12050						12055					12060			

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Ile Pro Ser Ser Thr Ala Ala Thr Val Pro Phe Met Val Pro Phe  
 12065 12070 12075  
 Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met  
 12080 12085 12090  
 Arg His Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Glu Leu  
 12095 12100 12105  
 Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr  
 12110 12115 12120  
 Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp  
 12125 12130 12135  
 Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp  
 12140 12145 12150  
 Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu  
 12155 12160 12165  
 Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu  
 12170 12175 12180  
 Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser  
 12185 12190 12195  
 Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly  
 12200 12205 12210  
 Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Ala Ala Gly  
 12215 12220 12225  
 Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu  
 12230 12235 12240  
 Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn  
 12245 12250 12255  
 Thr Met Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys  
 12260 12265 12270  
 Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu  
 12275 12280 12285  
 Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile  
 12290 12295 12300



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Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu  
 12305 12310 12315  
 Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu  
 12320 12325 12330  
 Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly  
 12335 12340 12345  
 Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr  
 12350 12355 12360  
 Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser  
 12365 12370 12375  
 Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe Thr  
 12380 12385 12390  
 Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly  
 12395 12400 12405  
 His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln  
 12410 12415 12420  
 Gly Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu  
 12425 12430 12435  
 Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu Lys Asp Gly  
 12440 12445 12450  
 Ala Ala Thr Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro  
 12455 12460 12465  
 Lys Ser Pro Gly Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser  
 12470 12475 12480  
 Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp  
 12485 12490 12495  
 Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val  
 12500 12505 12510  
 Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr  
 12515 12520 12525  
 Ser Gly Thr Pro Phe Ser Leu Pro Ser Pro Ala Thr Ala Gly Pro

12530 022438.43867(pct2).ST25.txt  
 12535 12540  
 Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys  
 12545 12550 12555  
 Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr  
 12560 12565 12570  
 Thr Glu Arg Val Leu Gln Thr Leu Leu Gly Pro Met Phe Lys Asn  
 12575 12580 12585  
 Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu  
 12590 12595 12600  
 Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys  
 12605 12610 12615  
 Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln  
 12620 12625 12630  
 Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu  
 12635 12640 12645  
 Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe  
 12650 12655 12660  
 Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser  
 12665 12670 12675  
 Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro  
 12680 12685 12690  
 Thr Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr  
 12695 12700 12705  
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser  
 12710 12715 12720  
 Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly  
 12725 12730 12735  
 Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys  
 12740 12745 12750  
 Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly  
 12755 12760 12765

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Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly  
12770 12775 12780

Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn  
12785 12790 12795

Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu  
12800 12805 12810

Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser  
12815 12820 12825

Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro  
12830 12835 12840

Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro  
12845 12850 12855

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp  
12860 12865 12870

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val  
12875 12880 12885

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly  
12890 12895 12900

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys  
12905 12910 12915

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu  
12920 12925 12930

Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu  
12935 12940 12945

Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr  
12950 12955 12960

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr  
12965 12970 12975

Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu  
12980 12985 12990

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala  
12995 13000 13005

022438.43867(pct2).ST25.txt

Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn  
 13010 13015 13020  
 Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe  
 13025 13030 13035  
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe  
 13040 13045 13050  
 Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr  
 13055 13060 13065  
 Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala  
 13070 13075 13080  
 Ile Cys Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg  
 13085 13090 13095  
 Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys  
 13100 13105 13110  
 Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn  
 13115 13120 13125  
 Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr Pro Gly  
 13130 13135 13140  
 Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu  
 13145 13150 13155  
 Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu  
 13160 13165 13170  
 Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Arg His  
 13175 13180 13185  
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly  
 13190 13195 13200  
 Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr  
 13205 13210 13215  
 Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala  
 13220 13225 13230  
 Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln  
 13235 13240 13245

022438.43867(pct2).ST25.txt

Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln  
 13250 13255 13260  
 Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg  
 13265 13270 13275  
 Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu  
 13280 13285 13290  
 Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser  
 13295 13300 13305  
 Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu  
 13310 13315 13320  
 Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr  
 13325 13330 13335  
 Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr  
 13340 13345 13350  
 Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser  
 13355 13360 13365  
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg  
 13370 13375 13380  
 Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu  
 13385 13390 13395  
 Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu  
 13400 13405 13410  
 Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly  
 13415 13420 13425  
 Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr  
 13430 13435 13440  
 His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr  
 13445 13450 13455  
 Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His  
 13460 13465 13470  
 Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr  
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13475 13480 13485

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser  
13490 13495 13500

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys  
13505 13510 13515

Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys  
13520 13525 13530

Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly  
13535 13540 13545

Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly  
13550 13555 13560

Leu Asp Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His  
13565 13570 13575

Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu  
13580 13585 13590

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser  
13595 13600 13605

Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro  
13610 13615 13620

Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro  
13625 13630 13635

Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn  
13640 13645 13650

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val  
13655 13660 13665

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly  
13670 13675 13680

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys  
13685 13690 13695

His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val  
13700 13705 13710

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Asp Pro 13715	Ile Gly Pro Gly 13720	Leu Asp Arg Glu Arg 13725	Tyr Trp Glu
Leu Ser 13730	Gln Leu Thr Asn Ser 13735	Ile Thr Glu Leu Gly 13740	Pro Tyr Thr
Leu Asp 13745	Arg Asp Ser Leu Tyr 13750	Val Asn Gly Phe Asn 13755	Pro Arg Ser
Ser Val 13760	Pro Thr Thr Ser Thr 13765	Pro Gly Thr Ser Thr 13770	Val His Leu
Ala Thr 13775	Ser Gly Thr Pro Ser 13780	Ser Leu Pro Gly His 13785	Thr Ala Pro
Val Pro 13790	Leu Leu Ile Pro Phe 13795	Thr Leu Asn Phe Thr 13800	Ile Thr Asn
Leu His 13805	Tyr Glu Glu Asn Met 13810	Gln His Pro Gly Ser 13815	Arg Lys Phe
Asn Thr 13820	Thr Glu Arg Val Leu 13825	Gln Gly Leu Leu Lys 13830	Pro Leu Phe
Lys Asn 13835	Thr Ser Val Gly Pro 13840	Leu Tyr Ser Gly Cys 13845	Arg Leu Thr
Leu Leu 13850	Arg Pro Glu Lys His 13855	Glu Ala Ala Thr Gly 13860	Val Asp Thr
Ile Cys 13865	Thr His Arg Val Asp 13870	Pro Ile Gly Pro Gly 13875	Leu Asp Arg
Glu Xaa 13880	Leu Tyr Trp Glu Leu 13885	Ser Xaa Leu Thr Xaa 13890	Xaa Ile Xaa
Glu Leu 13895	Gly Pro Tyr Xaa Leu 13900	Asp Arg Xaa Ser Leu 13905	Tyr Val Asn
Gly Phe 13910	Xaa Xaa Xaa Xaa Xaa 13915	Xaa Xaa Xaa Thr Ser 13920	Thr Pro Gly
Thr Ser 13925	Xaa Val Xaa Leu Xaa 13930	Thr Ser Gly Thr Pro 13935	Xaa Xaa Xaa
Pro Xaa 13940	Xaa Thr Ser Ala Gly 13945	Pro Leu Leu Val Pro 13950	Phe Thr Leu

022438.43867(pct2).ST25.txt

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His  
 13955 13960 13965  
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly  
 13970 13975 13980  
 Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr  
 13985 13990 13995  
 Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asn Gly Ala  
 14000 14005 14010  
 Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu Asp Pro Lys  
 14015 14020 14025  
 Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln  
 14030 14035 14040  
 Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg  
 14045 14050 14055  
 Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala  
 14060 14065 14070  
 Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser  
 14075 14080 14085  
 Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro Leu  
 14090 14095 14100  
 Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr  
 14105 14110 14115  
 Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr  
 14120 14125 14130  
 Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser  
 14135 14140 14145  
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg  
 14150 14155 14160  
 Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr  
 14165 14170 14175  
 His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu  
 14180 14185 14190



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Tyr Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly  
 14195 14200 14205  
 Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr  
 14210 14215 14220  
 His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr  
 14225 14230 14235  
 Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro  
 14240 14245 14250  
 Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr  
 14255 14260 14265  
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser  
 14270 14275 14280  
 Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser  
 14285 14290 14295  
 Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys  
 14300 14305 14310  
 Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly  
 14315 14320 14325  
 Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly  
 14330 14335 14340  
 Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His  
 14345 14350 14355  
 Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu  
 14360 14365 14370  
 Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg  
 14375 14380 14385  
 Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro  
 14390 14395 14400  
 Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Val Leu  
 14405 14410 14415  
 Phe Thr Ile Asn Cys Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp  
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14420 14425 14430

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val  
14435 14440 14445

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly  
14450 14455 14460

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys  
14465 14470 14475

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu  
14480 14485 14490

Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu  
14495 14500 14505

Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr  
14510 14515 14520

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser  
14525 14530 14535

Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu  
14540 14545 14550

Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser Ser Pro Thr Ile Met  
14555 14560 14565

Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile  
14570 14575 14580

Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg  
14585 14590 14595

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro  
14600 14605 14610

Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg  
14615 14620 14625

Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val  
14630 14635 14640

Asp Ala Ala Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu  
14645 14650 14655

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Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser  
14660 14665 14670

Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Val Ser Leu Tyr  
14675 14680 14685

Val Asn Gly Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr  
14690 14695 14700

Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser  
14705 14710 14715

Ser Leu Pro Gly His Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe  
14720 14725 14730

Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met  
14735 14740 14745

Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu  
14750 14755 14760

Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr  
14765 14770 14775

Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp  
14780 14785 14790

Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp  
14795 14800 14805

Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu  
14810 14815 14820

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu  
14825 14830 14835

Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser  
14840 14845 14850

Phe Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly  
14855 14860 14865

Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly  
14870 14875 14880

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu  
14885 14890 14895

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Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Arg Phe Asn  
 14900 14905 14910  
 Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe Lys  
 14915 14920 14925  
 Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu  
 14930 14935 14940  
 Leu Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile  
 14945 14950 14955  
 Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu  
 14960 14965 14970  
 Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu  
 14975 14980 14985  
 Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly  
 14990 14995 15000  
 Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr  
 15005 15010 15015  
 Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro  
 15020 15025 15030  
 Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn  
 15035 15040 15045  
 Phe Thr Ile Thr Asp Leu His Tyr Glu Glu Asn Met Gln His Pro  
 15050 15055 15060  
 Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu  
 15065 15070 15075  
 Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser  
 15080 15085 15090  
 Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala  
 15095 15100 15105  
 Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly  
 15110 15115 15120  
 Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu  
 15125 15130 15135

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Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp  
 15140 15145 15150  
 Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr  
 15155 15160 15165  
 Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly  
 15170 15175 15180  
 Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu  
 15185 15190 15195  
 Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu  
 15200 15205 15210  
 Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Ser Thr Thr Glu  
 15215 15220 15225  
 Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser  
 15230 15235 15240  
 Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro  
 15245 15250 15255  
 Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr His  
 15260 15265 15270  
 Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr  
 15275 15280 15285  
 Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro  
 15290 15295 15300  
 Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly Phe Thr His  
 15305 15310 15315  
 Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser Thr Met  
 15320 15325 15330  
 His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro Thr  
 15335 15340 15345  
 Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile  
 15350 15355 15360  
 Thr Asn Gln Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg  
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15365 15370 15375

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro  
15380 15385 15390

Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg  
15395 15400 15405

Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val  
15410 15415 15420

Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu  
15425 15430 15435

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser  
15440 15445 15450

Ile Thr Glu Leu Gly Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr  
15455 15460 15465

Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile  
15470 15475 15480

Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala  
15485 15490 15495

Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val Pro Phe  
15500 15505 15510

Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met  
15515 15520 15525

Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu  
15530 15535 15540

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro  
15545 15550 15555

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg  
15560 15565 15570

Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp  
15575 15580 15585

Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu  
15590 15595 15600

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Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu  
 15605 15610 15615

Asp Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Thr Ser  
 15620 15625 15630

Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly  
 15635 15640 15645

Thr Ser Gly Thr Pro Phe Ser Leu Pro Ser Pro Ala Xaa Xaa Xaa  
 15650 15655 15660

Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu  
 15665 15670 15675

Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn  
 15680 15685 15690

Thr Thr Glu Arg Val Leu Gln Thr Leu Leu Gly Pro Met Phe Lys  
 15695 15700 15705

Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu  
 15710 15715 15720

Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile  
 15725 15730 15735

Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu  
 15740 15745 15750

Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu  
 15755 15760 15765

Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly  
 15770 15775 15780

Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr  
 15785 15790 15795

Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Leu Pro Ser Ser  
 15800 15805 15810

Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe  
 15815 15820 15825

Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly  
 15830 15835 15840

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Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu  
 15845 15850 15855  
 Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly  
 15860 15865 15870  
 Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr  
 15875 15880 15885  
 Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro  
 15890 15895 15900  
 Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr  
 15905 15910 15915  
 Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser  
 15920 15925 15930  
 Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr  
 15935 15940 15945  
 Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr  
 15950 15955 15960  
 Pro Ser Ser Leu Pro Ser Pro Thr Xaa Xaa Xaa Pro Leu Leu Xaa  
 15965 15970 15975  
 Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu  
 15980 15985 15990  
 Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg  
 15995 16000 16005  
 Val Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val  
 16010 16015 16020  
 Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu  
 16025 16030 16035  
 Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa  
 16040 16045 16050  
 Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp  
 16055 16060 16065  
 Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr  
 16070 16075 16080



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Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Trp  
 16085 16090 16095  
 Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp  
 16100 16105 16110  
 Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala  
 16115 16120 16125  
 Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn  
 16130 16135 16140  
 Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe  
 16145 16150 16155  
 Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly Pro Met Phe  
 16160 16165 16170  
 Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
 16175 16180 16185  
 Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala  
 16190 16195 16200  
 Ile Cys Thr His Arg Val Asp Pro Lys Ser Pro Gly Val Asp Arg  
 16205 16210 16215  
 Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys  
 16220 16225 16230  
 Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn  
 16235 16240 16245  
 Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly  
 16250 16255 16260  
 Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu  
 16265 16270 16275  
 Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu  
 16280 16285 16290  
 Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His  
 16295 16300 16305  
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly  
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16310		16315		16320										
Leu	Leu	Gly	Pro	Met	Phe	Lys	Asn	Thr	Ser	Val	Gly	Leu	Leu	Tyr
16325						16330					16335			
Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asn	Gly	Ala
16340						16345					16350			
Ala	Thr	Gly	Met	Asp	Ala	Ile	Cys	Thr	His	Arg	Leu	Asp	Pro	Lys
16355						16360					16365			
Ser	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa
16370						16375					16380			
Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg
16385						16390					16395			
Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
16400						16405					16410			
Xaa	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Xaa	Val	Xaa	Leu	Xaa	Thr	Ser
16415						16420					16425			
Gly	Thr	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Pro	Leu
16430						16435					16440			
Leu	Xaa	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Xaa	Tyr
16445						16450					16455			
Glu	Glu	Xaa	Met	Xaa	Xaa	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
16460						16465					16470			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Lys	Pro	Leu	Phe	Arg	Asn	Ser
16475						16480					16485			
Ser	Leu	Glu	Tyr	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Ala	Ser	Leu	Arg
16490						16495					16500			
Pro	Glu	Lys	Asp	Ser	Ser	Ala	Met	Ala	Val	Asp	Ala	Ile	Cys	Thr
16505						16510					16515			
His	Arg	Pro	Asp	Pro	Glu	Asp	Leu	Gly	Leu	Asp	Arg	Glu	Arg	Leu
16520						16525					16530			
Tyr	Trp	Glu	Leu	Ser	Asn	Leu	Thr	Asn	Gly	Ile	Gln	Glu	Leu	Gly
16535						16540					16545			

022438.43867(pct2).ST25.txt

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr  
 16550 16555 16560  
 His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr  
 16565 16570 16575  
 Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro  
 16580 16585 16590  
 Thr Thr Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr  
 16595 16600 16605  
 Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly Ser  
 16610 16615 16620  
 Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly  
 16625 16630 16635  
 Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys  
 16640 16645 16650  
 Arg Leu Thr Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly  
 16655 16660 16665  
 Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly  
 16670 16675 16680  
 Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn  
 16685 16690 16695  
 Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu  
 16700 16705 16710  
 Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser  
 16715 16720 16725  
 Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro  
 16730 16735 16740  
 Phe Ser Leu Pro Ser Pro Ala Thr Ala Gly Pro Leu Leu Val Leu  
 16745 16750 16755  
 Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp  
 16760 16765 16770  
 Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val  
 16775 16780 16785

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Leu Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly  
 16790 16795 16800  
 Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys  
 16805 16810 16815  
 Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu  
 16820 16825 16830  
 Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu  
 16835 16840 16845  
 Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa  
 16850 16855 16860  
 Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa  
 16865 16870 16875  
 Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu  
 16880 16885 16890  
 Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa  
 16895 16900 16905  
 Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn  
 16910 16915 16920  
 Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe  
 16925 16930 16935  
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe  
 16940 16945 16950  
 Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
 16955 16960 16965  
 Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala  
 16970 16975 16980  
 Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg  
 16985 16990 16995  
 Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr  
 17000 17005 17010  
 Glu Leu Gly Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn  
 17015 17020 17025

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Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly  
 17030 17035 17040  
 Thr Ser Ala Val His Leu Glu Thr Thr Gly Thr Pro Ser Ser Phe  
 17045 17050 17055  
 Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe  
 17060 17065 17070  
 Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His  
 17075 17080 17085  
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly  
 17090 17095 17100  
 Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr  
 17105 17110 17115  
 Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala  
 17120 17125 17130  
 Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile  
 17135 17140 17145  
 Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln  
 17150 17155 17160  
 Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg  
 17165 17170 17175  
 Asp Ser Leu Tyr Val Asp Gly Phe Asn Pro Trp Ser Ser Val Pro  
 17180 17185 17190  
 Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser  
 17195 17200 17205  
 Gly Thr Pro Ser Pro Leu Pro Gly His Thr Ala Pro Val Pro Leu  
 17210 17215 17220  
 Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asp Leu His Tyr  
 17225 17230 17235  
 Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr  
 17240 17245 17250  
 Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr  
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17255 17260 17265

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg  
17270 17275 17280

Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr  
17285 17290 17295

Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu  
17300 17305 17310

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly  
17315 17320 17325

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn  
17330 17335 17340

Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr  
17345 17350 17355

Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His  
17360 17365 17370

Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr  
17375 17380 17385

Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly Ser  
17390 17395 17400

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu His Gly  
17405 17410 17415

Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys  
17420 17425 17430

Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly  
17435 17440 17445

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly  
17450 17455 17460

Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa  
17465 17470 17475

Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu  
17480 17485 17490

022438.43867(pct2).ST25.txt

Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser  
 17495 17500 17505  
 Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro  
 17510 17515 17520  
 Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro  
 17525 17530 17535  
 Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa  
 17540 17545 17550  
 Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val  
 17555 17560 17565  
 Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly  
 17570 17575 17580  
 Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys  
 17585 17590 17595  
 Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa  
 17600 17605 17610  
 Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu  
 17615 17620 17625  
 Leu Ser Xaa Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr  
 17630 17635 17640  
 Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser  
 17645 17650 17655  
 Ser Met Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu  
 17660 17665 17670  
 Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro  
 17675 17680 17685  
 Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn  
 17690 17695 17700  
 Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe  
 17705 17710 17715  
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe  
 17720 17725 17730

022438.43867(pct2).ST25.txt

Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr  
 17735 17740 17745  
 Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr  
 17750 17755 17760  
 Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg  
 17765 17770 17775  
 Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa  
 17780 17785 17790  
 Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn  
 17795 17800 17805  
 Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly  
 17810 17815 17820  
 Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa  
 17825 17830 17835  
 Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu  
 17840 17845 17850  
 Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa  
 17855 17860 17865  
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly  
 17870 17875 17880  
 Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr  
 17885 17890 17895  
 Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala  
 17900 17905 17910  
 Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa  
 17915 17920 17925  
 Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa  
 17930 17935 17940  
 Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg  
 17945 17950 17955  
 Xaa Ser Leu Tyr Val Asn Gly Phe His Pro Arg Ser Ser Val Pro  
 17960 17965 17970



022438.43867(pct2).ST25.txt

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser  
 17975 17980 17985  
 Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu  
 17990 17995 18000  
 Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr  
 18005 18010 18015  
 Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr  
 18020 18025 18030  
 Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr  
 18035 18040 18045  
 Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg  
 18050 18055 18060  
 Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser  
 18065 18070 18075  
 His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Xaa Leu  
 18080 18085 18090  
 Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly  
 18095 18100 18105  
 Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa  
 18110 18115 18120  
 Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa  
 18125 18130 18135  
 Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa  
 18140 18145 18150  
 Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr  
 18155 18160 18165  
 Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser  
 18170 18175 18180  
 Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Xaa  
 18185 18190 18195  
 Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys

022438.43867(pct2).ST25.txt

18200	18205	18210									
Arg	Leu	Thr	Leu	Leu	Arg	Xaa	Glu	Lys	Xaa	Xaa	Ala
18215						18220					18225
											Ala
											Thr
											Xaa
Val	Asp	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Asp	Pro	Xaa
18230						18235					18240
											Xaa
											Pro
											Gly
Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa
18245						18250					18255
											Leu
											Thr
											Xaa
Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg
18260						18265					18270
											Xaa
											Ser
											Leu
Tyr	Val	Asn	Gly	Phe	Thr	His	Gln	Asn	Ser	Val	Pro
18275						18280					18285
											Thr
											Thr
											Ser
Thr	Pro	Gly	Thr	Ser	Thr	Val	Tyr	Trp	Ala	Thr	Thr
18290						18295					18300
											Gly
											Thr
											Pro
Ser	Ser	Phe	Pro	Gly	His	Thr	Glu	Pro	Gly	Pro	Leu
18305						18310					18315
											Leu
											Ile
											Pro
Phe	Thr	Phe	Asn	Phe	Thr	Ile	Thr	Asn	Leu	His	Tyr
18320						18325					18330
											Glu
											Glu
											Asn
Met	Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
18335						18340					18345
											Glu
											Arg
											Val
Leu	Gln	Gly	Leu	Leu	Thr	Pro	Leu	Phe	Lys	Asn	Thr
18350						18355					18360
											Ser
											Val
											Gly
Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
18365						18370					18375
											Pro
											Glu
											Lys
Gln	Glu	Ala	Ala	Thr	Gly	Val	Asp	Thr	Ile	Cys	Thr
18380						18385					18390
											His
											Arg
											Val
Asp	Pro	Ile	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu
18395						18400					18405
											Tyr
											Trp
											Glu
Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly
18410						18415					18420
											Pro
											Tyr
											Xaa
Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Xaa
18425						18430					18435
											Xaa
											Xaa
											Xaa

022438.43867(pct2).ST25.txt

Xaa Xaa	Xaa Xaa Thr Ser Thr	Pro Gly Thr Ser Xaa	Val Xaa Leu
18440	18445	18450	
Xaa Thr	Ser Gly Thr Pro Xaa	Xaa Xaa Pro Xaa Xaa	Thr Xaa Xaa
18455	18460	18465	
Xaa Pro	Leu Leu Xaa Pro Phe	Thr Leu Asn Phe Thr	Ile Thr Asn
18470	18475	18480	
Leu Xaa	Tyr Glu Glu Xaa Met	Xaa Xaa Pro Gly Ser	Arg Lys Phe
18485	18490	18495	
Asn Thr	Thr Glu Arg Val Leu	Gln Gly Leu Leu Xaa	Pro Xaa Phe
18500	18505	18510	
Lys Xaa	Thr Ser Val Gly Xaa	Leu Tyr Ser Gly Cys	Arg Leu Thr
18515	18520	18525	
Leu Leu	Arg Xaa Glu Lys Xaa	Xaa Ala Ala Thr Xaa	Val Asp Xaa
18530	18535	18540	
Xaa Cys	Xaa Xaa Xaa Xaa Asp	Pro Xaa Xaa Pro Gly	Leu Asp Arg
18545	18550	18555	
Glu Xaa	Leu Tyr Trp Glu Leu	Ser Xaa Leu Thr Xaa	Xaa Ile Xaa
18560	18565	18570	
Glu Leu	Gly Pro Tyr Xaa Leu	Asp Arg Xaa Ser Leu	Tyr Val Asn
18575	18580	18585	
Gly Phe	Thr His Arg Ser Ser	Val Pro Thr Thr Ser	Ser Pro Gly
18590	18595	18600	
Thr Ser	Thr Val His Leu Ala	Thr Ser Gly Thr Pro	Ser Ser Leu
18605	18610	18615	
Pro Gly	His Thr Ala Pro Val	Pro Leu Leu Ile Pro	Phe Thr Leu
18620	18625	18630	
Asn Phe	Thr Ile Thr Asn Leu	His Tyr Glu Glu Asn	Met Gln His
18635	18640	18645	
Pro Gly	Ser Arg Lys Phe Asn	Thr Thr Glu Arg Val	Leu Gln Gly
18650	18655	18660	
Leu Leu	Lys Pro Leu Phe Lys	Ser Thr Ser Val Gly	Pro Leu Tyr
18665	18670	18675	

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Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala  
 18680 18685 18690  
 Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr  
 18695 18700 18705  
 Gly Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa  
 18710 18715 18720  
 Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg  
 18725 18730 18735  
 Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 18740 18745 18750  
 Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser  
 18755 18760 18765  
 Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu  
 18770 18775 18780  
 Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr  
 18785 18790 18795  
 Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr  
 18800 18805 18810  
 Glu Arg Val Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr  
 18815 18820 18825  
 Ser Val Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg  
 18830 18835 18840  
 Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa  
 18845 18850 18855  
 Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu  
 18860 18865 18870  
 Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly  
 18875 18880 18885  
 Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr  
 18890 18895 18900  
 His Arg Thr Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr  
 18905 18910 18915

022438.43867(pct2).ST25.txt

Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His  
 18920 18925 18930  
 Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr  
 18935 18940 18945  
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser  
 18950 18955 18960  
 Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Ser  
 18965 18970 18975  
 Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys  
 18980 18985 18990  
 Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly  
 18995 19000 19005  
 Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly  
 19010 19015 19020  
 Leu Asp Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His  
 19025 19030 19035  
 Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu  
 19040 19045 19050  
 Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser  
 19055 19060 19065  
 Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro  
 19070 19075 19080  
 Ser Ser Phe Pro Gly His Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro  
 19085 19090 19095  
 Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa  
 19100 19105 19110  
 Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val  
 19115 19120 19125  
 Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly  
 19130 19135 19140  
 Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys  
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19145	19150	19155							
Xaa Xaa	Ala Ala Thr Xaa Val	Asp Xaa Xaa Cys Xaa	Xaa Xaa Xaa						
19160	19165	19170							
Asp Pro	Xaa Xaa Pro Gly Leu	Asp Arg Glu Xaa Leu	Tyr Trp Glu						
19175	19180	19185							
Leu Ser	Xaa Leu Thr Xaa Xaa	Ile Xaa Glu Leu Gly	Pro Tyr Xaa						
19190	19195	19200							
Leu Asp	Arg Xaa Ser Leu Tyr	Val Asn Gly Phe Thr	His Trp Ser						
19205	19210	19215							
Ser Gly	Leu Thr Thr Ser Thr	Pro Trp Thr Ser Thr	Val Asp Leu						
19220	19225	19230							
Gly Thr	Ser Gly Thr Pro Ser	Pro Val Pro Ser Pro	Thr Thr Ala						
19235	19240	19245							
Gly Pro	Leu Leu Val Pro Phe	Thr Leu Asn Phe Thr	Ile Thr Asn						
19250	19255	19260							
Leu Gln	Tyr Glu Glu Asp Met	His Arg Pro Gly Ser	Arg Lys Phe						
19265	19270	19275							
Asn Ala	Thr Glu Arg Val Leu	Gln Gly Leu Leu Ser	Pro Ile Phe						
19280	19285	19290							
Lys Asn	Thr Ser Val Gly Pro	Leu Tyr Ser Gly Cys	Arg Leu Thr						
19295	19300	19305							
Leu Leu	Arg Pro Glu Lys Gln	Glu Ala Ala Thr Gly	Val Asp Thr						
19310	19315	19320							
Ile Cys	Thr His Arg Val Asp	Pro Ile Gly Pro Gly	Leu Asp Arg						
19325	19330	19335							
Glu Xaa	Leu Tyr Trp Glu Leu	Ser Xaa Leu Thr Xaa	Xaa Ile Xaa						
19340	19345	19350							
Glu Leu	Gly Pro Tyr Xaa Leu	Asp Arg Xaa Ser Leu	Tyr Val Asn						
19355	19360	19365							
Gly Phe	Xaa Xaa Xaa Xaa Xaa	Xaa Xaa Xaa Thr Ser	Thr Pro Gly						
19370	19375	19380							

022438.43867(pct2).ST25.txt

Thr	Ser	Xaa	Val	Xaa	Leu	Xaa	Thr	Ser	Gly	Thr	Pro	Xaa	Xaa	Xaa
19385						19390					19395			
Pro	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Pro	Leu	Leu	Xaa	Pro	Phe	Thr	Leu
19400						19405					19410			
Asn	Phe	Thr	Ile	Thr	Asn	Leu	Xaa	Tyr	Glu	Glu	Xaa	Met	Xaa	Xaa
19415						19420					19425			
Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly
19430						19435					19440			
Leu	Leu	Xaa	Pro	Xaa	Phe	Lys	Xaa	Thr	Ser	Val	Gly	Xaa	Leu	Tyr
19445						19450					19455			
Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Xaa	Glu	Lys	Xaa	Xaa	Ala
19460						19465					19470			
Ala	Thr	Xaa	Val	Asp	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Asp	Pro	Xaa
19475						19480					19485			
Xaa	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa
19490						19495					19500			
Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg
19505						19510					19515			
Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Phe	Gly	Leu
19520						19525					19530			
Thr	Thr	Ser	Thr	Pro	Trp	Thr	Ser	Thr	Val	Asp	Leu	Gly	Thr	Ser
19535						19540					19545			
Gly	Thr	Pro	Ser	Pro	Val	Pro	Ser	Pro	Thr	Thr	Ala	Gly	Pro	Leu
19550						19555					19560			
Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr
19565						19570					19575			
Glu	Glu	Asp	Met	His	Arg	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
19580						19585					19590			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Thr	Pro	Leu	Phe	Arg	Asn	Thr
19595						19600					19605			
Ser	Val	Ser	Ser	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
19610						19615					19620			

022438.43867(pct2).ST25.txt

Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr  
 19625 19630 19635  
 His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Xaa Leu  
 19640 19645 19650  
 Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly  
 19655 19660 19665  
 Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa  
 19670 19675 19680  
 Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa  
 19685 19690 19695  
 Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa  
 19700 19705 19710  
 Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr  
 19715 19720 19725  
 Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser  
 19730 19735 19740  
 Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Xaa  
 19745 19750 19755  
 Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys  
 19760 19765 19770  
 Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa  
 19775 19780 19785  
 Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly  
 19790 19795 19800  
 Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa  
 19805 19810 19815  
 Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu  
 19820 19825 19830  
 Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser  
 19835 19840 19845  
 Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser  
 19850 19855 19860



022438.43867(pct2).ST25.txt

Ser Leu 19865 Pro Ser Pro Thr Thr 19870 Ala Gly Pro Leu Leu 19875 Val Pro Phe  
 Thr Leu 19880 Asn Phe Thr Ile Thr 19885 Asn Leu Gln Tyr Gly 19890 Glu Asp Met  
 Gly His 19895 Pro Gly Ser Arg Lys 19900 Phe Asn Thr Thr Glu 19905 Arg Val Leu  
 Gln Gly 19910 Leu Leu Gly Pro Ile 19915 Phe Lys Asn Thr Ser 19920 Val Gly Pro  
 Leu Tyr 19925 Ser Gly Cys Arg Leu 19930 Thr Ser Leu Arg Ser 19935 Glu Lys Asp  
 Gly Ala 19940 Ala Thr Gly Val Asp 19945 Ala Ile Cys Ile His 19950 His Leu Asp  
 Pro Lys 19955 Ser Pro Gly Leu Asp 19960 Arg Glu Xaa Leu Tyr 19965 Trp Glu Leu  
 Ser Xaa 19970 Leu Thr Xaa Xaa Ile 19975 Xaa Glu Leu Gly Pro 19980 Tyr Xaa Leu  
 Asp Arg 19985 Xaa Ser Leu Tyr Val 19990 Asn Gly Phe Xaa Xaa 19995 Xaa Xaa Xaa  
 Xaa Xaa 20000 Xaa Thr Ser Thr Pro 20005 Gly Thr Ser Xaa Val 20010 Xaa Leu Xaa  
 Thr Ser 20015 Gly Thr Pro Xaa Xaa 20020 Xaa Pro Xaa Xaa Thr 20025 Xaa Xaa Xaa  
 Pro Leu 20030 Leu Xaa Pro Phe Thr 20035 Leu Asn Phe Thr Ile 20040 Thr Asn Leu  
 Xaa Tyr 20045 Glu Glu Xaa Met Xaa 20050 Xaa Pro Gly Ser Arg 20055 Lys Phe Asn  
 Thr Thr 20060 Glu Arg Val Leu Gln 20065 Gly Leu Leu Xaa Pro 20070 Xaa Phe Lys  
 Xaa Thr 20075 Ser Val Gly Xaa Leu 20080 Tyr Ser Gly Cys Arg 20085 Leu Thr Leu  
 Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa

20090 022438.43867(pct2).ST25.txt  
 20095 20100

Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu  
 20105 20110 20115

Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu  
 20120 20125 20130

Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly  
 20135 20140 20145

Phe Thr His Gln Thr Phe Ala Pro Asn Thr Ser Thr Pro Gly Thr  
 20150 20155 20160

Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro  
 20165 20170 20175

Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn  
 20180 20185 20190

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro  
 20195 20200 20205

Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu  
 20210 20215 20220

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser  
 20225 20230 20235

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala  
 20240 20245 20250

Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser  
 20255 20260 20265

Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu  
 20270 20275 20280

Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa  
 20285 20290 20295

Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20300 20305 20310

Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly  
 20315 20320 20325

022438.43867(pct2).ST25.txt

Thr	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Thr	Ala	Pro	Val	Pro	Leu	Leu
20330						20335					20340			
Ile	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	His	Tyr	Glu
20345						20350					20355			
Glu	Asn	Met	Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu
20360						20365					20370			
Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Ser	Thr	Ser
20375						20380					20385			
Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro
20390						20395					20400			
Glu	Lys	His	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	Leu
20405						20410					20415			
Arg	Leu	Asp	Pro	Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Arg	Leu	Tyr
20420						20425					20430			
Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Ser	Val	Thr	Glu	Leu	Gly	Pro
20435						20440					20445			
Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	Gln
20450						20455					20460			
Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile	Pro	Gly	Thr	Ser	Ala	Val
20465						20470					20475			
His	Leu	Glu	Thr	Ser	Gly	Thr	Pro	Ala	Ser	Leu	Pro	Gly	His	Thr
20480						20485					20490			
Ala	Pro	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile
20495						20500					20505			
Thr	Asn	Leu	Gln	Tyr	Glu	Val	Asp	Met	Arg	His	Pro	Gly	Ser	Arg
20510						20515					20520			
Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Lys	Pro
20525						20530					20535			
Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg
20540						20545					20550			
Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Arg	Gly	Ala	Ala	Thr	Gly	Val
20555						20560					20565			

022438.43867(pct2).ST25.txt

Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu  
 20570 20575 20580  
 Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly  
 20585 20590 20595  
 Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr  
 20600 20605 20610  
 Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr  
 20615 20620 20625  
 Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser  
 20630 20635 20640  
 Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Val Pro Phe  
 20645 20650 20655  
 Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Ala Met  
 20660 20665 20670  
 Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu  
 20675 20680 20685  
 Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Ile Gly Pro  
 20690 20695 20700  
 Leu Ty Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp  
 20705 20710 20715  
 Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro Asp  
 20720 20725 20730  
 Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu  
 20735 20740 20745  
 Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu  
 20750 20755 20760  
 Asp Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His Trp Ser Pro  
 20765 20770 20775  
 Ile Pro Thr Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu Gly  
 20780 20785 20790  
 Thr Ser Gly Ile Pro Pro Ser Leu Pro Glu Thr Thr Xaa Xaa Xaa  
 20795 20800 20805

022438.43867(pct2).ST25.txt

Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu  
 20810 20815 20820  
 Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn  
 20825 20830 20835  
 Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys  
 20840 20845 20850  
 Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu  
 20855 20860 20865  
 Leu Arg Pro Glu Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile  
 20870 20875 20880  
 Cys Thr His Arg Pro Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln  
 20885 20890 20895  
 Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu  
 20900 20905 20910  
 Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly  
 20915 20920 20925  
 Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr  
 20930 20935 20940  
 Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro Ser Ser Leu Pro  
 20945 20950 20955  
 Gly Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn  
 20960 20965 20970  
 Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro  
 20975 20980 20985  
 Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu  
 20990 20995 21000  
 Leu Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser  
 21005 21010 21015  
 Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala  
 21020 21025 21030  
 Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser  
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21035 022438.43867(pct2).ST25.txt  
 21040 21045  
 Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu  
 21050 21055 21060  
 Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His  
 21065 21070 21075  
 Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr  
 21080 21085 21090  
 Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg  
 21095 21100 21105  
 Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu  
 21110 21115 21120  
 Val Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu  
 21125 21130 21135  
 Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu  
 21140 21145 21150  
 Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser  
 21155 21160 21165  
 Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro  
 21170 21175 21180  
 Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr  
 21185 21190 21195  
 Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr  
 21200 21205 21210  
 Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro  
 21215 21220 21225  
 Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Asn Val Gly Phe Thr Gln  
 21230 21235 21240  
 Arg Ser Ser Val Pro Thr Thr Ser Val Pro Gly Thr Pro Thr Val  
 21245 21250 21255  
 Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser  
 21260 21265 21270

022438.43867(pct2).ST25.txt

Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Gly Thr Ile  
 21275 21280 21285

Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg  
 21290 21295 21300

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Ser  
 21305 21310 21315

Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg  
 21320 21325 21330

Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val  
 21335 21340 21345

Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu  
 21350 21355 21360

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn  
 21365 21370 21375

Ile Thr Glu Leu Gly His Tyr Ala Leu Asp Asn Asp Ser Leu Phe  
 21380 21385 21390

Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr  
 21395 21400 21405

Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala  
 21410 21415 21420

Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe  
 21425 21430 21435

Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met  
 21440 21445 21450

Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln  
 21455 21460 21465

Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu  
 21470 21475 21480

Tyr Ser Gly Ser Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly  
 21485 21490 21495

Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro  
 21500 21505 21510

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Thr Gly 21515	Pro Gly Leu Asp Arg 21520	Glu Gln Leu Tyr Leu 21525	Glu Leu Ser
Gln Leu 21530	Thr His Ser Ile Thr 21535	Glu Leu Gly Pro Tyr 21540	Thr Leu Asp
Arg Asp 21545	Ser Leu Tyr Val Asn 21550	Gly Phe Thr His Arg 21555	Ser Ser Val
Pro Thr 21560	Thr Ser Thr Gly Val 21565	Val Ser Glu Glu Pro 21570	Phe Thr Leu
Asn Phe 21575	Thr Ile Asn Asn Leu 21580	Arg Tyr Met Ala Asp 21585	Met Gly Gln
Pro Gly 21590	Ser Leu Lys Phe Asn 21595	Ile Thr Asp Asn Val 21600	Met Lys His
Leu Leu 21605	Ser Pro Leu Phe Gln 21610	Arg Ser Ser Leu Gly 21615	Ala Arg Tyr
Thr Gly 21620	Cys Arg Val Ile Ala 21625	Leu Arg Ser Val Lys 21630	Asn Gly Ala
Glu Thr 21635	Arg Val Asp Leu Leu 21640	Cys Thr Tyr Leu Gln 21645	Pro Leu Ser
Gly Pro 21650	Gly Leu Pro Ile Lys 21655	Gln Val Phe His Glu 21660	Leu Ser Gln
Gln Thr 21665	His Gly Ile Thr Arg 21670	Leu Gly Pro Tyr Ser 21675	Leu Asp Lys
Asp Ser 21680	Leu Tyr Leu Asn Gly 21685	Tyr Asn Glu Pro Gly 21690	Leu Asp Glu
Pro Pro 21695	Thr Thr Pro Lys Pro 21700	Ala Thr Thr Phe Leu 21705	Pro Pro Leu
Ser Glu 21710	Ala Thr Thr Ala Met 21715	Gly Tyr His Leu Lys 21720	Thr Leu Thr
Leu Asn 21725	Phe Thr Ile Ser Asn 21730	Leu Gln Tyr Ser Pro 21735	Asp Met Gly
Lys Gly 21740	Ser Ala Thr Phe Asn 21745	Ser Thr Glu Gly Val 21750	Leu Gln His



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Leu Leu Arg Pro Leu. Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr  
 21755 21760 21765  
 Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala  
 21770 21775 21780  
 Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val  
 21785 21790 21795  
 Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln  
 21800 21805 21810  
 Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg  
 21815 21820 21825  
 Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile  
 21830 21835 21840  
 Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu  
 21845 21850 21855  
 Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg  
 21860 21865 21870  
 Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu  
 21875 21880 21885  
 His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp  
 21890 21895 21900  
 Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp  
 21905 21910 21915  
 Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala  
 21920 21925 21930  
 Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His  
 21935 21940 21945  
 Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser  
 21950 21955 21960  
 Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro  
 21965 21970 21975  
 Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg  
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